

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 16, 2002, 11:43:18 ; Search time 66 Seconds
(without alignments)
69.699 Million cell updates/sec

Title: US-09-648-389A-1

Perfect score: 15

Sequence: 1 cttggccgctgccat 15

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/2/1na/5A.COMB.seq:*
2: /cgn2_6/ptodata/2/1na/5B.COMB.seq:*
3: /cgn2_6/ptodata/2/1na/6A.COMB.seq:*
4: /cgn2_6/ptodata/2/1na/6B.COMB.seq:*
5: /cgn2_6/ptodata/2/1na/PTCUS.COMB.seq:*
6: /cgn2_6/ptodata/2/1na/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	15	4	US-09-142-779-4
2	15	100.0	843	1	US-08-040-548-9
3	15	100.0	843	1	US-08-466-344-9
4	15	100.0	3068	2	US-08-224-482-1
5	15	100.0	3086	1	US-08-040-548-15
6	15	100.0	3086	1	US-08-466-344-15
7	15	100.0	3086	6	5206152-1
8	13.4	89.3	25	2	US-08-626-169-12
9	13.4	89.3	25	3	US-09-164-907-12
10	13.4	89.3	612	2	US-08-760-075A-15
11	13.4	89.3	612	4	US-09-338-546-15
12	13.4	89.3	612	4	US-09-659-084-15
13	13.4	89.3	724	4	US-08-858-207A-206
14	13.4	89.3	1920	2	US-08-855-714-1
15	13.4	89.3	2291	1	US-07-872-644-5
16	13.4	89.3	2291	1	US-08-297-494-5
17	13.4	89.3	2291	1	US-08-297-510-5
18	13.4	89.3	2291	1	US-08-479-532-5
19	13.4	89.3	2291	1	US-08-455-526-5
20	13.4	89.3	2291	1	US-08-455-526-5
21	13.4	89.3	2291	3	US-09-139-491-5
22	13.4	89.3	2291	5	PCR-US92-03222-5
23	13.4	89.3	2656	1	US-07-872-644-16
24	13.4	89.3	2656	1	US-08-297-494-16
25	13.4	89.3	2656	1	US-08-297-510-16
26	13.4	89.3	2656	1	US-08-479-532-16
27	13.4	89.3	2656	1	US-08-455-526-16

28	13.4	89.3	2656	1	US-08-455-525-16	Sequence 16, Appl
29	13.4	89.3	2656	3	US-09-139-491-16	Sequence 16, Appl
30	13.4	89.3	2656	5	PCR-US92-03222-16	Sequence 16, Appl
31	13.4	89.3	2781	1	US-08-178-477B-42	Sequence 42, Appl
32	13.4	89.3	3132	2	US-08-224-482-3	Sequence 3, Appl
33	13.4	89.3	3132	3	US-09-205-921-1	Sequence 1, Appl
34	13.4	89.3	3539	3	US-08-936-135-7	Sequence 7, Appl
35	13.4	89.3	4718	3	US-08-936-135-9	Sequence 9, Appl
36	13.4	89.3	4733	3	US-08-936-135-11	Sequence 11, Appl
37	13.4	89.3	4765	3	US-08-936-135-21	Sequence 21, Appl
38	13.4	89.3	4769	3	US-08-936-135-13	Sequence 13, Appl
39	13.4	89.3	4772	4	US-09-484-970B-133	Sequence 133, Appl
40	13.4	89.3	4780	3	US-08-936-135-23	Sequence 23, Appl
41	13.4	89.3	4784	3	US-08-936-135-15	Sequence 15, Appl
42	13.4	89.3	28171	4	US-08-961-5527-22	Sequence 22, Appl
43	13.4	89.3	4403765	4	US-09-103-840A-2	Sequence 2, Appl
44	13	86.7	25	4	US-09-257-583-30	Sequence 30, Appl
45	13	86.7	614	2	US-07-625-334-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-09-142-779-4
Sequence 4, Application US/09142779B
Patent No. 6200960
GENERAL INFORMATION:
APPLICANT: Knachigian, Levon M.
TITLE OF INVENTION: Inhibition of Proliferation of Cells
FILE REFERENCE: 273402002000
CURRENT APPLICATION NUMBER: US/09/142,779B
CURRENT FILING DATE: 1999-04-13
EARLIER FILING DATE: 1996-03-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 15
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide
US-09-142-779-4

Query Match 100.0%; Score 15; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 CTTGGCCGCTGCCAT 15

RESULT 2
US-08-040-548-9/c
Sequence 9, Application US/08040548
Patent No. 5763209
GENERAL INFORMATION:
APPLICANT: Sukhatme, Vikas P.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE
TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: 321 No. 5763209th Clark Street, Suite 800
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60610
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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/ TITLE OF INVENTION: Molecular Toxicology Modeling
/ FILE REFERENCE: 44921-5038-US
/ CURRENT APPLICATION NUMBER: US/09/917,800A
/ CURRENT FILING DATE: 2001-07-31
/ PRIOR APPLICATION NUMBER: US 60/222,040
/ PRIOR FILING DATE: 2000-07-31
/ PRIOR APPLICATION NUMBER: US 60/222,880
/ PRIOR FILING DATE: 2000-11-02
/ PRIOR APPLICATION NUMBER: US 60/290,029
/ PRIOR FILING DATE: 2001-05-11
/ PRIOR APPLICATION NUMBER: US 60/290,645
/ PRIOR FILING DATE: 2001-05-15
/ PRIOR APPLICATION NUMBER: US 60/292,336
/ PRIOR FILING DATE: 2001-05-22
/ PRIOR APPLICATION NUMBER: US 60/295,798
/ PRIOR FILING DATE: 2001-06-06
/ PRIOR APPLICATION NUMBER: US 60/297,457
/ PRIOR FILING DATE: 2001-06-13
/ PRIOR APPLICATION NUMBER: US 60/298,884
/ PRIOR FILING DATE: 2001-06-19
/ PRIOR APPLICATION NUMBER: US 60/303,459
/ PRIOR FILING DATE: 2001-07-09
/ NUMBER OF SEQ ID NOS: 1740
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1543
/ LENGTH: 3112
/ TYPE: DNA
/ ORGANISM: Rattus norvegicus
/ FEATURE:
/ OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_012551
US-09-917-800A-1543

Query Match          100.0%; Score 15; DB 10; Length 3112;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGGCCGCTGCCAT 15
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DB 283 CTTGGCCGCTGCCAT 269

RESULT 3
US-09-974-300-5464/C
/ Sequence 5464, Application US/09974300
/ Patent No. US20020146721A1
/ GENERAL INFORMATION:
/ APPLICANT: Berka, Randy M.
/ APPLICANT: Clausen, Ib Groth
/ TITLE OF INVENTION: Methods For Monitoring Multiple Gene
/ TITLE OF INVENTION: Expression
/ FILE REFERENCE: 10085, 500-US
/ CURRENT APPLICATION NUMBER: US/09/974,300
/ CURRENT FILING DATE: 2001-10-05
/ PRIOR APPLICATION NUMBER: 09/680,598
/ PRIOR FILING DATE: 2000-10-06
/ PRIOR APPLICATION NUMBER: 60/279,526
/ PRIOR FILING DATE: 2001-03-27
/ NUMBER OF SEQ ID NOS: 8481
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 5464
/ LENGTH: 152
/ TYPE: DNA
/ ORGANISM: Bacillus clausii
US-09-974-300-5464

Query Match          89.3%; Score 13.4; DB 10; Length 152;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY 1 CTTGGCCGCTGCCAT 15
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DB 49 CTTGGCCGCTGCCAT 35
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RESULT 4
US-09-864-761-27552
/ Sequence 27552, Application US/09864761
/ Patent No. US20020048763A1
/ GENERAL INFORMATION:
/ APPLICANT: Penn, Sharon G.
/ APPLICANT: Rank, David R.
/ APPLICANT: Hanzel, David K.
/ APPLICANT: Chen, Wensheng
/ TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
/ TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
/ FILE REFERENCE: Aecm1ca-X-1
/ CURRENT APPLICATION NUMBER: US/09/864,761
/ CURRENT FILING DATE: 2001-05-23
/ PRIOR APPLICATION NUMBER: US 60/180,312
/ PRIOR FILING DATE: 2000-02-04
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: US 09/632,366
/ PRIOR FILING DATE: 2000-08-03
/ PRIOR APPLICATION NUMBER: GB 24263,6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00662
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00661
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00670
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: 09/774,203
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: US 09/608,408
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: US 60/234,687
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: US 09/774,203
/ PRIOR FILING DATE: 2001-01-29
/ NUMBER OF SEQ ID NOS: 49117
/ SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
/ SEQ ID NO 27552
/ LENGTH: 157
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: MAP TO AC003108.1
/ OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
/ OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
/ OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
/ OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
/ OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
/ OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
/ OTHER INFORMATION: NT HIT: M64229.1, EVALUE 2.30e-02
/ OTHER INFORMATION: EST_HUMAN HIT: BE85401.1, EVALUE 2.00e-83
US-09-864-761-27552

Query Match          89.3%; Score 13.4; DB 10; Length 157;
Best Local Similarity 93.3%; Pred. No. 2.5e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Arnold, White & Durkee
;; STREET: 321 No. 5763209th Clark Street, Suite 800
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: U.S.A.
;; ZIP: 60610
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent Release #1.0, Version #1.25
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/040,548
;; FILING DATE:
;; CLASSIFICATION: 514
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Coughlin, Daniel F.
;; REGISTRATION NUMBER: 36,111
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 744-0090
;; TELEFAX: (312) 245-4961
;;
;; INFORMATION FOR SEQ ID NO: 15:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3086 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; US-08-040-548-15
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Query Match 100.0%; Score 15; DB 1; Length 3086;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CTTGGCCGCTGCCAT 15
Db 273 CTTGGCCGCTGCCAT 259
;
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;; RESULT 6
;; US-08-466-344-15/C
;; Sequence 15, Application US/08466344
;; Patent No. 5773583
;; GENERAL INFORMATION:
;; APPLICANT: Sukhatme, Vikas P.
;; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE
;; TITLE OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS
;; NUMBER OF SEQUENCES: 67
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Arnold, White & Durkee
;; STREET: 321 No. 5773583th Clark Street, Suite 800
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: U.S.A.
;; ZIP: 60610
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent Release #1.0, Version #1.25
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/466,344
;; FILING DATE: 06-JUN-1995
;; CLASSIFICATION: 514
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/040,548
;; FILING DATE: 31-MAR-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Coughlin, Daniel F.
;; REGISTRATION NUMBER: 36,111
;; REFERENCE/DOCKET NUMBER: arcd067
;;

;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 744-0090
;; TELEFAX: (312) 245-4961
;; INFORMATION FOR SEQ ID NO: 15:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3086 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; US-08-466-344-15
;
Query Match 100.0%; Score 15; DB 1; Length 3086;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CTTGGCCGCTGCCAT 15
Db 273 CTTGGCCGCTGCCAT 259
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;;
;; RESULT 7
;; 5206152-1/C
;; Patent No. 5206152
;; APPLICANT: SUKHATME,VIKAS P.
;; TITLE OF INVENTION: CLONING AND EXPRESSION OF EARLY GROWTH
;; REGULATORY PROTEIN GENES
;; NUMBER OF SEQUENCES: 18
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/249,584
;; FILING DATE: 26-SEP-1988
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 179,587
;; FILING DATE: 08-APR-1988
;; SEQ ID NO:11
;; LENGTH: 3086
;; 5206152-1
;
Query Match 100.0%; Score 15; DB 6; Length 3086;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CTTGGCCGCTGCCAT 15
Db 273 CTTGGCCGCTGCCAT 259
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;;
;; RESULT 8
;; US-08-626-169-12/C
;; Sequence 12, Application US/08626169
;; Patent No. 5661248
;; GENERAL INFORMATION:
;; APPLICANT: Russell, David W.
;; TITLE OF INVENTION: Thapsen, Anice E.
;; TITLE OF INVENTION: BIOMARKERS FOR DETECTION, DIAGNOSIS
;; NUMBER OF SEQUENCES: 19
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Arnold, White & Durkee
;; STREET: P.O. Box 4433
;; CITY: Houston
;; STATE: Texas
;; COUNTRY: United States
;; ZIP: 77210
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent Release #1.0, Version #1.30
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/626,169
;; FILING DATE: Concurrently Herewith
;; CLASSIFICATION: 435
;;

OTHER INFORMATION: SWISSPROT HIT: P48651, EVALUE 6.80e+00
OTHER INFORMATION: NT HIT: X74507.1, EVALUE 6.10e-01
US-09-864-761-31839

Query Match
Best Local Similarity 89.3%; Score 13.4; DB 10; Length 255;
93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTGGCCGCTGCCAT 15
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DB 66 CTTGGCCTGCTGCCAT 52

RESULT 7
US-09-923-876-2313/c
Sequence 2313, Application US/09923876
Patent No. US20020013958A1

GENERAL INFORMATION:
APPLICANT: Laligudi, Raghunath V.
APPLICANT: Kamigaki, Laura Y. (Ito)

APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING

FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: US/09/923,876
PRIOR FILING DATE: 2001-08-06

PRIOR APPLICATION NUMBER: 09/298,329
PRIOR FILING DATE: 1999-04-21

PRIOR APPLICATION NUMBER: 60/085,331
PRIOR FILING DATE: 1998-05-05

NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PERL Program

SEQ ID NO 2313
LENGTH: 265

TYPE: DNA
ORGANISM: Zea mays

FEATURE:
NAME/KEY: misc.feature

OTHER INFORMATION: Incyte ID No. US20020013958A1 700160401H1
LOCATION: 48

OTHER INFORMATION: a, t, c, g, or other
US-09-923-876-2313

Query Match
Best Local Similarity 89.3%; Score 13.4; DB 10; Length 265;
93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTGGCCGCTGCCAT 15
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DB 70 CTTGGCCTGCTGCCAT 56

RESULT 8
US-09-923-876-4805/c

Sequence 4805, Application US/09923876
Patent No. US20020013958A1

GENERAL INFORMATION:
APPLICANT: Laligudi, Raghunath V.
APPLICANT: Kamigaki, Laura Y. (Ito)

APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING

FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: US/09/923,876

PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: 09/298,329

PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/085,331

NUMBER OF SEQ ID NOS: 6332
SOFTWARE: PERL Program

SEQ ID NO 4805
LENGTH: 273

TYPE: DNA

ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No. US20020013958A1 700455822H1
US-09-923-876-4805

Query Match
Best Local Similarity 89.3%; Score 13.4; DB 10; Length 273;
93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTGGCCGCTGCCAT 15
||||| |||||
DB 270 CTTGGCCTGCTGCCAT 256

RESULT 9
US-09-960-352-4856/c
Sequence 4856, Application US/09960352
Patent No. US20020137139A1

GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengping

APPLICANT: Byatt, John C.
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352

CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112

SEQ ID NO 4856
LENGTH: 349

TYPE: DNA
ORGANISM: Bos taurus

OTHER INFORMATION: Clone ID: 21-LIB34-001-Q1-E1-F9
US-09-960-352-4856

Query Match
Best Local Similarity 89.3%; Score 13.4; DB 10; Length 349;
93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTGGCCGCTGCCAT 15
||||| |||||
DB 48 CTTGGCCGCTGCCAT 34

RESULT 10
US-09-960-352-11961/c
Sequence 11961, Application US/09960352
Patent No. US20020137139A1

GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengping

APPLICANT: Byatt, John C.
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND

FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352

CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112

SEQ ID NO 11961
LENGTH: 414

TYPE: DNA
ORGANISM: Bos taurus

OTHER INFORMATION: Clone ID: 51-LIB34-004-Q1-E1-E4
US-09-960-352-11961

Query Match
Best Local Similarity 89.3%; Score 13.4; DB 10; Length 414;
93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTGGCCGCTGCCAT 15

ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/309
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 612 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..612
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1..612
US-09-338-546-15

Query Match
Best Local Similarity 89.3%; Score 13.4; DB 4; Length 612;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTGCCCGCTGCCAT 15
Db 339 CTTGCCCGCTGCACAT 325

RESULT 12
US-09-659-084-15/c
Sequence 15, Application US/09659084
Patent No. 6403299

GENERAL INFORMATION:
APPLICANT: KIRSCHBAUM, Bernd
MODELNER, Stefan
BARTLETT, Robert
TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/659,084
FILING DATE: 11-Sep-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/338,546
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/309
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 612 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..612
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1..612
US-09-659-084-15

Query Match
Best Local Similarity 89.3%; Score 13.4; DB 4; Length 612;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTGCCCGCTGCCAT 15
Db 339 CTTGCCCGCTGCACAT 325

RESULT 13
US-08-858-207A-206
Sequence 206, Application US/08858207A
Patent No. 6348328

GENERAL INFORMATION:
APPLICANT: Black, Michael
Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Nicholas, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328e1 Compounds
NUMBER OF SEQUENCES: 552
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,207A
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimm, Edward R.
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50475
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 206:
SEQUENCE CHARACTERISTICS:
LENGTH: 724 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-858-207A-206

Query Match
Best Local Similarity 89.3%; Score 13.4; DB 4; Length 724;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTGCCCGCTGCCAT 15
Db 367 CTTGCCCGCTGCACAT 381

PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 16568
LENGTH: 454
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC007263.3
OTHER INFORMATION: EXPRESSED IN BR474, SIGNAL = 0.64
US-09-864-761-16568

Query Match 89.3%; Score 13.4; DB 10; Length 454;
Best Local Similarity 93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGGCCGCTGCCAT 15
Db 346 CTGGCTGCTGCCAT 332

RESULT 14
US-09-864-761-10916
Sequence 10916, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aesomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 10916
LENGTH: 480
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC003108.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
US-09-864-761-10916

Query Match 89.3%; Score 13.4; DB 10; Length 480;
Best Local Similarity 93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTGGCCGCTGCCAT 15
Db 413 CTGGCAGCTGCCAT 427

RESULT 15
US-09-974-300-5449/c
Sequence 5449, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berra, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
FILE REFERENCE: 10085,500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5449
LENGTH: 489
TYPE: DNA
ORGANISM: Bacillus clausii
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(489)
OTHER INFORMATION: n = A,T,C or G
US-09-974-300-5449

Query Match 89.3%; Score 13.4; DB 10; Length 489;

CC Vascular cells, preferably smooth muscle or endothelial cells or cells
 involved in neoplasia.

XX Sequence 4321 BP; 908 A; 1308 C; 1106 G; 999 T; 0 other;

Query Match 100.0%; Score 15; DB 21; Length 4321;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGGCCGCTGCCAT 15
 |||||||
 DB 828 CTTGGCCGCTGCCAT 814

RESULT 13
 AAF85131/C
 ID AAF85131 standard; DNA; 4321 BP.

XX AAF85131;

AC 09-JUL-2001 (first entry)

DT Nucleotide sequence of rat early growth response factor-1.

XX Early growth response factor; EGR, tumour cell; tumour; DNazyme;
 XX Antisense oligonucleotide; prostate tumour; hepatocellular carcinoma;
 XX Skin carcinoma; breast tumour; ss.

OS Rattus rattus.

XX WO20010394-A1.

PN 03-MAY-2001.

PD 26-OCT-2000; 2000WO-AU01315.

XX 26-OCT-1999; 99AU-0003676.

XX (UNIX) UNISEARCH LTD.

XX Khachigian LM;

DR WPI: 2001-300428/31.

XX Treating tumors including prostate tumour, breast tumour, skin carcinoma,
 PT comprising administering agent which inhibits induction or decreases
 PT expression of early growth response factor-1

XX Disclosure: Page 16-23; 80pp; English.

XX The present sequence represents an early growth response factor-1
 CC (EGR-1) DNA sequence. The specification describes a method for
 CC inhibiting the growth or proliferation of a tumour cell and treating
 CC tumors. The method comprises contacting a tumour cell or administering
 CC to a subject, an agent which inhibits induction, decreases expression
 CC or which decreases the nuclear accumulation or activity of EGR. The
 CC agent is a DNazyme or an antisense oligonucleotide. The method is
 CC useful for treating solid tumors, including prostate tumours,
 CC hepatocellular carcinoma, skin carcinoma or breast tumours.

XX Sequence 4321 BP; 908 A; 1308 C; 1106 G; 999 T; 0 other;

Query Match 100.0%; Score 15; DB 22; Length 4321;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGGCCGCTGCCAT 15
 |||||||
 DB 828 CTTGGCCGCTGCCAT 814

RESULT 14
 AB199867/c

ID AB199867 standard; CDNA; 4494 BP.

XX AB199867;

AC 07-MAR-2002 (first entry)

DT Mouse ischemic condition related CDNA sequence SEQ ID NO:1002.

XX Mouse; ischemia; compressive ischemia; occlusive ischemia;
 XX vasospastic ischemia; ischemic condition; ischemic disease; ss.

XX Mus musculus.

XX WO20018188-A2.

PN 22-NOV-2001.

PD 18-MAY-2001; 2001WO-JP04192.

XX 18-MAY-2000; 2000JP-0145977.

XX (YUNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.

XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;

DR WPI: 2002-034733/04.

XX P-PSDB; ABB57356.

XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring
 PT expression levels of particular genes defined in the specification or
 PT by determining the expression profile of a gene group comprising these
 PT genes

XX Claim 2: Page 2532-2537; 2690pp; English.

XX The present invention describes a method for examining ischemic
 CC conditions, comprising measuring the expression levels of particular
 CC genes (I) in a test sample or determining the expression profile of a
 CC gene group in the sample comprising genes selected from (I). The method
 CC is useful for examining the ischemic condition (e.g. compressive
 CC ischemia, occlusive ischemia or vasospastic ischemia) by measuring
 CC expression levels of particular genes (AB199202 to AB199912, encoding
 CC the protein sequences in ABB57020 to ABB57374) or by determining the
 CC expression profile of a gene group comprising these genes. The
 CC expression levels or expression profiles produced by these genes are
 CC used as an indicator when screening for ischemic condition-improving
 CC drugs or therapeutics for ischemic diseases. AB19913 and AB19914
 CC represent PCR primers for a mouse ischemic condition related sequence,
 CC which are used in the exemplification of the present invention.

XX Sequence 4494 BP; 940 A; 1417 C; 1163 G; 974 T; 0 other;

Query Match 100.0%; Score 15; DB 24; Length 4494;
 Best Local Similarity 100.0%; Pred. No. 2.6e+02;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGGCCGCTGCCAT 15
 |||||||
 DB 1692 CTTGGCCGCTGCCAT 1678

RESULT 15

ABN17030/c
 ID ABN17030 standard; CDNA; 501 BP.

XX ABN17030;

AC 24-JUN-2002 (first entry)

XX Human ORFX polynucleotide sequence SEQ ID NO:2537.

XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
 KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;

encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library Genome Res. 11 (2), 281-289 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for
further details.

e mouse tissues.

FEATURES

source

Location/Qualifiers

```
1..459
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_id="RIKEN full-length enriched, pooled cell lines"
/note="Pooled cell lines ; (cell_line=RCB-0035 WEHI-3),
(cell_line=CRL-2116 JC), (cell_line=RCB-0035 WEHI-3),
(cell_line=RCB-0464 Meth-A), (cell_line=RCB-0545 OHTA),
(cell_line=RCB-0559 K-1.F1), (cell_line=RCB-1283 B16
melanoma), (cell_type=B cells, cell_line=CRL-1702 WEHI 231
), (cell_type=Leydig cells, cell_line=CRL-2065 MTC-1),
(cell_type=Nullipotent stem cell, cell_line=CRL-2070 NE),
(tissue_type=bladder, cell_line=RCB-0544 MBr-2),
(tissue_type=bone marrow, cell_type=stroma cell,
cell_line=CRL-2028 SR-4987), (tissue_type=colon,
cell_line=RCB-0549 C1e-H3), (tissue_type=kidney,
cell_line=CCL-142 RAG), (tissue_type=submandibular gland,
cell_line=CRL-1734 SCA-9 clone 15), (strain=BALB/C,
cell_type=B cells, cell_line=CRL-1669 BCL1 Clone 13.20-3b3
), (strain=C3H, tissue_type=brain, cell_line=CRL-1443
BC3H1)"
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BASE COUNT 82 a 172 c 136 g 69 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 15; DB 10; Length 459;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTTGGCCGCTGCCAT 15

Db 300 CTTGGCCGCTGCCAT 286

Search completed: December 16, 2002, 14:15:28
Job time : 2426 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 16, 2002, 11:04:08 : Search time 303 Seconds

(Without alignments)
11.485 Million cell updates/sec

Title: US-09-648-389A-1

Perfect score: 15

Sequence: 1 ctggccgcgtccat 15

Scoring table:

IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

N.Geneseq.101002:*

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- 2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
- 3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
- 4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
- 5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
- 6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
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- 12: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*
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- 20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
- 21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
- 22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
- 23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	15	100.0	15 18 AAT90567	Antisense sequence
2	15	100.0	15 21 AAAT74448	Antisense sequence
3	15	100.0	15 22 AAF85119	Antisense oligonuc
4	15	100.0	15 22 AAF85133	Antisense oligonuc
5	15	100.0	843 15 AAO73457	Egr-1 transcriptio
6	15	100.0	3068 20 AAAT64275	Mouse Egr-1 CDNA
7	15	100.0	3068 21 AAAT74395	Mouse Egr-1 coding
8	15	100.0	3068 22 AAF85130	Nucleotide sequenc
9	15	100.0	3086 10 AAN91815	Egr-1-contg. OC3.1

10	15	100.0	3086 15 AAO73463	Mouse Egr-1 clone
11	15	100.0	3112 24 ABR63636	Rat sequence diffe
12	15	100.0	4321 21 AAAT74396	Rat Egr-1 coding s
13	15	100.0	4321 22 AAF85131	Nucleotide sequenc
14	15	100.0	4494 24 ABN199867	Mouse ischaemic co
15	14	93.3	501 24 ABN17030	Human ORFX polyunc
16	14	93.3	987 23 AAS92184	DNA encoding novel
17	14	93.3	1566 21 AAC42849	Arabidopsis thalia
18	14	93.3	2100 22 AAH66705	C glutamicum codin
19	14	93.3	2223 22 AAF71483	Corynebacterium g1
20	14	93.3	2350 22 AAS15846	C. glutamicum pat
21	14	93.3	2588 21 AAC76756	Human OREF ORF2311
22	14	93.3	3192 22 AAL04902	Human reproductive
23	14	93.3	3192 23 ABL04903	Human testicular a
24	14	93.3	3192 23 ABL97796	Human testicular a
25	14	93.3	3192 23 ABL97797	Drosophila melanog
26	14	93.3	3479 23 ABL06683	Drosophila melanog
27	14	93.3	4108 22 AAF99988	DNA encoding Coryn
28	14	93.3	6995 22 AAF25332	Nucleotide sequenc
29	14	93.3	6995 22 AAF29332	C. glutamicum Opca
30	14	93.3	9863 23 ABL20890	Drosophila melanog
31	14	93.3	13497 23 ABL03557	Drosophila melanog
32	14	93.3	13497 23 ABL03557	Drosophila melanog
33	14	93.3	15464 23 ABL06682	Drosophila melanog
34	14	93.3	16489 23 ABL03556	Drosophila melanog
35	14	93.3	349980 22 AAH68529	C glutamicum codin
36	13.4	89.3	25 18 AAT89069	Identification of
37	13.4	89.3	152 24 ABR78173	Bacillus clausii g
38	13.4	89.3	157 22 ABR70430	Human foetal liver
39	13.4	89.3	157 22 AAK18671	Human brain expres
40	13.4	89.3	157 22 AAK44600	Human bone marrow
41	13.4	89.3	157 22 AAI50582	Probe #19268 used
42	13.4	89.3	157 24 ABS18838	Human genome-deriv
43	13.4	89.3	174 21 AAC20671	Human secreted pro
44	13.4	89.3	197 22 AAL19770	Human breast cance
45	13.4	89.3	200 22 AAL19820	Human breast cance

ALIGNMENTS

RESULT 1
AAT90567
ID AAT90567 standard; DNA; 15 BP.
XX AAT90567;
AC
XX
XX 24-MAR-1998 (first entry)
XX
XX Antisense sequence A/S2 directed against Egr-1.
DE
XX Antisense sequence; Inhibitor; Egr-1; rat; early growth response gene;
XX cellular proliferation; Inhibitor; cell migration inhibition; therapy;
KW
KW atherosclerosis; restenosis; ss.
XX
XX Synthetic.
OS
OS Rattus sp.
OS
XX WO9732979-A1.
XX
XX 12-SEP-1997.
XX
XX 07-MAR-1997; 97WO-AU00140.
XX
XX 07-MAR-1996; 96AU-0008554.
XX
XX (UNIX) UNISEARCH LTD.
XX
XX Khachigian LM;
XX
XX WPI; 1997-470545/43.
XX
XX Inhibiting cell proliferation by altering Egr-1 levels - useful in

transcriptional activator
 JOURNAL Mol. Cell. Biol. 10 (7), 3456-3467 (1990)
 MEDLINE 90287135
 PUBMED 2113174
 FEATURES
 source location/Qualifiers
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 BASE COUNT 60 a 170 c 103 g 57 t
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 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTGGCCGCTGCCAT 15
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 Db 309 CTTGGCCGCTGCCAT 295
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 LOCUS RNRKRX1 676 bp mRNA linear ROD 27-JUL-2000
 DEFINITION Rattus norvegicus Krox-24 mRNA, partial cds.
 ACCESSION U75398
 VERSION U75398.1 GI:1732257
 KEYWORDS
 SEGMENT 1 of 2
 SOURCE Rattus norvegicus.
 ORGANISM Rattus norvegicus
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 676)
 Adams, L.D., Lemire, J.M. and Schwartz, S.M.
 A systematic analysis of 40 random genes in cultured vascular
 smooth muscle subtypes reveals a heterogeneity of gene expression
 and identifies the tight junction gene zonula occludens 2 as a
 marker of epithelioid 'pup' smooth muscle cells and a participant
 in carotid neointimal formation
 Arterioscler. Thromb. Vasc. Biol. 19 (11), 2600-2608 (1999)
 JOURNAL MEDLINE 20027749
 PUBMED 10559001
 REFERENCE 2 (bases 1 to 676)
 AUTHORS Adams, L.A., Merry, I. and Schwartz, S.M.
 TITLE Direct Submision
 JOURNAL Submitted (18-OCT-1996) Pathology, University of Washington, 1959
 NE Pacific, Seattle, WA 98195, USA
 FEATURES
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 /dev_stage="two day old pup"
 1..331
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 332..>676
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 /protein_id="AAB38708.1"

/db_xref="GI:1732260"
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 BASE COUNT 133 a 258 c 179 g 100 t 6 others.
 ORIGIN
 Query Match 100.0%; Score 15; DB 10; Length 676;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTGGCCGCTGCCAT 15
 |||||||
 Db 262 CTTGGCCGCTGCCAT 248
 RESULT 3
 LOCUS AR012087/c 843 bp DNA linear PAT 04-DEC-1998
 DEFINITION Sequence 9 from patent US 5763209.
 ACCESSION AR012087
 VERSION AR012087.1 GI:3970077
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE Unclassified.
 AUTHORS 1 (bases 1 to 843)
 TITLE Sukhame, V.P.
 JOURNAL Methods and materials relating to the functional domains of DNA
 binding proteins
 Patent: US 5763209-A 9 09-JUN-1998;
 FEATURES
 source location/Qualifiers
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 BASE COUNT 172 a 299 c 209 g 163 t
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 Query Match 100.0%; Score 15; DB 6; Length 843;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTGGCCGCTGCCAT 15
 |||||||
 Db 15 CTTGGCCGCTGCCAT 1
 RESULT 4
 LOCUS AR014526/c 843 bp DNA linear PAT 05-DEC-1998
 DEFINITION Sequence 9 from patent US 5773583.
 ACCESSION AR014526
 VERSION AR014526.1 GI:3971980
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE Unclassified.
 AUTHORS 1 (bases 1 to 843)
 TITLE Sukhame, V.P.
 JOURNAL Methods and materials relating to the functional domains of DNA
 binding proteins
 Patent: US 5773583-A 9 30-JUN-1998;
 FEATURES
 source location/Qualifiers
 1..843
 /organism="unknown"
 BASE COUNT 172 a 299 c 209 g 163 t
 ORIGIN
 Query Match 100.0%; Score 15; DB 6; Length 843;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTGGCCGCTGCCAT 15
 |||||||

```

      DB      1 CTTGCCCGCTGCCAT 15
      |||||
RESULT 4
AA073457/c
ID AAF85133 standard; DNA; 15 BP.
XX
XX AAF85133;
XX
XX 09-JUL-2001 (first entry)
XX
XX Antisense oligonucleotide which targets an EGR-1 gene.
XX
XX Early growth response factor; EGR; tumour cell; tumour; DNase;
XX antisense oligonucleotide; prostate tumour; hepatocellular carcinoma;
XX skin carcinoma; breast tumour; phosphorothioate; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 1..15
XX /tag= a
XX /note= "phosphorothioate-linked bases"
XX
XX WO200130394-A1.
XX
XX 03-MAY-2001.
XX
XX 26-OCT-2000; 2000WO-AU01315.
XX
XX 26-OCT-1999; 99AU-0003676.
XX
XX (UNIX ) UNISEARCH LTD.
XX
XX Khachigian LM;
XX
XX WPI; 2001-300428/31.
XX
XX Treating tumors including prostate tumour, breast tumour, skin carcinoma,
XX comprises administering agent which inhibits induction or decreases
XX expression of early growth response factor-1
XX
XX Example 1; Page 24; 80pp; English.
XX
XX The present sequence represents an antisense oligonucleotide, which
XX targets an early growth response factor (EGR) gene. The specification
XX describes a method for inhibiting the growth or proliferation of a tumour
XX cell and treating tumours. The method comprises contacting a tumour cell
XX or administering to a subject, an agent which inhibits induction,
XX decreases expression or which decreases the nuclear accumulation or
XX activity of EGR. The agent is a DNase or an antisense oligonucleotide.
XX The method is useful for treating solid tumours, including prostate
XX tumours, hepatocellular carcinoma, skin carcinoma or breast tumours.
XX
XX Sequence 15 BP; 1 A; 6 C; 4 G; 4 T; 0 other;
XX
Query Match 100.0%; Score 15; DB 22; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CTTGCCCGCTGCCAT 15
XX |||||
DB 1 CTTGCCCGCTGCCAT 15
XX
RESULT 5
AA073457/c
ID AAF85133 standard; DNA; 843 BP.
XX
XX AA073457;
XX
XX 06-MAY-1995 (first entry)
XX

```

```

XX DE Egr-1 transcription activator domain.
XX
XX XX Early growth regulatory protein; Egr-1; zinc finger;
XX DNA binding protein; cell growth; transcription activator;
XX nuclear localization; polynucleotide binding; ss.
XX
XX Mus sp.
XX
XX WO9423030-A.
XX
XX 13-OCT-1994.
XX
XX 10-MAR-1994; 94WO-US02611.
XX
XX 31-MAR-1993; 93US-0040548.
XX
XX (ARCH-) ARCH DEV CORP.
XX
XX Sukhame VP;
XX
XX WPI; 1994-333191/41.
XX
XX New early growth regulatory polypeptide and related DNA - useful
XX for modulating transcription, localisation and binding of
XX polynucleotide(s)
XX
XX Disclosure; Page 92; 145pp; English.
XX
XX Clone OCS.1 was isolated from a cDNA library derived from
XX BALB/c 3T3 mouse cells, and designated Egr-1. Particular domains of
XX Egr-1 protein have specific functions: activation of transcription
XX (domains given in AAF63131-32), repression of transcription
XX (AAF63133), nuclear localization (AAF63134-35), and polynucleotide
XX binding (AAF63136). DNA sequences AA073457-62 respectively encode
XX the peptides given in AAF63131-36. Virus and plasmid vectors
XX containing such sequences can be used (by transfection or
XX transformation) to regulate transcription in prokaryotic or
XX eukaryotic hosts.
XX
XX Sequence 843 BP; 172 A; 299 C; 209 G; 163 T; 0 other;
XX
Query Match 100.0%; Score 15; DB 15; Length 843;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CTTGCCCGCTGCCAT 15
XX |||||
DB 15 CTTGCCCGCTGCCAT 1
XX
RESULT 6
AAV64275/c
ID AAV64275 standard; DNA; 3068 BP.
XX
XX AAV64275;
XX
XX 27-JAN-1999 (first entry)
XX
XX Mouse Egr-1 cDNA.
XX
XX Egr-1; murine; early growth response protein; inhibitor; tumour; mitogen;
XX platelet-derived growth factor; PDGF; retroviral vector; osteosarcoma;
XX zinc finger domain; fibrosarcoma; glioblastoma; carcinoma; ds.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
XX CDS 370..1860
XX /tag= a
XX /product= "Egr-1"
XX
XX US5837692-A.
XX

```

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source
  1. 1983
  /organism="Mus musculus"
  /db_xref="taxon:10090"
  /map="18 bands C-D"
  /clone_1lb="cosmid clone 2/2"
  1185. 1971
  /gene="Krox-24"
  /note="minor transcription start site"
  /number=1
  protein_bind
    1254. 1261
    /gene="Krox-24"
    /bound_molety="Sp1"
    1325. 1330
    /gene="Krox-24"
    /bound_molety="Sp1"
    1366. 1370
    /gene="Krox-24"
    /bound_molety="AP1"
    1395. 1971
    /gene="Krox-24"
    /note="major transcription start site"
    /number=1
  exon
    352 a 687 c 630 g 314 t
  BASE COUNT
  ORIGIN
  Query Match
    Best Local Similarity 100.0%; Score 15; DB 10; Length 1983;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  Oy 1 CTTGCGCGCTGCCAT 15
  Db 1688 CTTGCGCGCTGCCAT 1674

RESULT 8
CHKFOA/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 2253)
Molders, H., Jenuwein, T., Adamkiewicz, J. and Muller, R.
Isolation and structural analysis of a biologically active chicken
c-fos cDNA: Identification of evolutionarily conserved domains in
fos protein
Oncogene 1 (4), 377-385 (1987)
JOURNAL
MEDLINE
PUBMED
FEATURES
source
  1. 2253
  /organism="Gallus gallus"
  /db_xref="taxon:9031"
  125. 1228
  /note="c-fos proto-oncogene product"
  /codon_start=1
  /protein_id="AA048670.1"
  /db_xref="GI:211470"
  /translation="MMIQFAGEYAEVSSRCSSASPAQDSLITYPPSPAFSSSGSPV
  NSQDFCTDLAVSSANFPTVTAISTPDLMVLOPTLISSVAASONGHGYAPAP
  PAAYSRPAVAKAGSGOSIGRGKYOLSPPEEKRIIRERKMAAACRNRRRL
  TDLQAEFTDLEEKSALEINILKEKLEETLAHAPACKMPPELAPSEELAA
  TALDLGAPPAALAEAFALPMTAPAPVAPKPKSGSLKAKAPPELLPSKPREA
  SRSPVMDLPGASSFVASDMEPIGAGSGGLPCTPVTCTPSPSTSTFVFTYPE
  ADAPSCAAAHRRGSSSNERSDSLSPFTLLAL"
  BASE COUNT
  ORIGIN
  399 a 729 c 647 g 478 t

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Query Match
  Best Local Similarity 100.0%; Score 15; DB 5; Length 2253;
  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  Oy 1 CTTGCGCGCTGCCAT 15
  Db 580 CTTGCGCGCTGCCAT 566

RESULT 9
GDFOS/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 2253)
Molders, H., Jenuwein, T., Adamkiewicz, J. and Muller, R.
Isolation and structural analysis of a biologically active chicken
c-fos cDNA: Identification of evolutionarily conserved domains in
fos protein
Oncogene (1987) In press
JOURNAL
FEATURES
source
  1. 2253
  /organism="Gallus gallus"
  /strain="SPAFAS"
  /db_xref="taxon:9031"
  /clone="1/1"
  /clone_1lb="pex 1"
  125. 1225
  /note="fos-protein"
  misc_feature
    399 a 729 c 647 g 478 t
  BASE COUNT
  ORIGIN
  Query Match
    Best Local Similarity 100.0%; Score 15; DB 5; Length 2253;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  Oy 1 CTTGCGCGCTGCCAT 15
  Db 580 CTTGCGCGCTGCCAT 566

RESULT 10
DVHRYWNGA
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 2700)
Corces, V.G.
Direct Submission
Submitted (01-JUL-1993) Corces V. G., The Johns Hopkins University,
Biology, 34th and Charles Sts, Baltimore, Maryland, USA, 21218
2 (bases 1 to 2700)
Harrison, D.A., Gdula, D.A., Coyne, R.S. and Corces, V.G.
A leucine zipper domain of the suppressor of Hairy-wing protein

```

```

XX PS Disclosure; Page 16-23; 80pp; English.
XX CC
XX CC The present sequence represents an early growth response factor-1
XX CC (Egr-1) DNA sequence. The specification describes a method for
XX CC inhibiting the growth or proliferation of a tumour cell and treating
XX CC tumours. The method comprises contacting a tumour cell or administering
XX CC to a subject, an agent which inhibits induction, decreases expression
XX CC or which decreases the nuclear accumulation or activity of EGR. The
XX CC agent is a DNAzyme or an antisense oligonucleotide. The method is
XX CC useful for treating solid tumours, including prostate tumours,
XX CC hepatocellular carcinoma, skin carcinoma or breast tumours.
XX
SQ Sequence 3068 BP; 688 A; 939 C; 705 G; 736 T; 0 other;

Query Match          100.0%; Score 15; DB 22; Length 3068;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGGCCCGCTGCCAT 15
   |||||
DB 273 CTTGGCCCGCTGCCAT 259

RESULT 9
ID AAN91815/c
XX AAN91815 standard; DNA; 3086 BP.
XX
AC AAN91815;
XX
DT 19-MAR-1990 (first entry)
XX
DE Egr-1-contg. OC3.1 clone.
XX
Egr-1; DNA-binding proteins; zinc fingers;
XX early growth regulatory proteins;
XX Mus.
OS
XX
FH Key Location/Qualifiers
FT mat_peptide 259..1857
FT /tag= a
FT polyA-signal 1865..1871
FT /tag= b
FT polyA-signal 3066..3072
FT /tag= c
FT polyA-signal 3053..3059
FT /tag= d
XX
PN WO8909777-A.
XX
PD 19-OCT-1989.
XX
PF 07-APR-1989; 89WO-US01473.
XX
PR 08-APR-1988; 88US-0179587.
XX
PR 26-SEP-1988; 88US-0249584.
XX
XX (ARCH-) ARCH DEVELOPMENT CORP.
XX
XX Sukhame VP;
XX PI
XX WPI; 1989-324195/44.
XX DR P-PSDB; AAR93113.
XX
XX Early growth regulatory proteins of mouse and human - including zinc
XX fingers, vectors and DNA sequence encoding the proteins, and methods
XX of detecting each.
XX
XX Claim 8; fig. 1.1-1.8; 55pp; English.
XX
XX The sequence is that of the OC3.1 clone contg. the mouse Egr-1 protein
XX sequence which has DNA-binding zinc fingers.

```

```

XX SQ Sequence 3086 BP; 706 A; 939 C; 705 G; 736 T; 0 other;
XX
XX Query Match          100.0%; Score 15; DB 10; Length 3086;
XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGGCCCGCTGCCAT 15
   |||||
DB 273 CTTGGCCCGCTGCCAT 259

RESULT 10
ID AAO73463/c
XX AAO73463 standard; cDNA; 3086 BP.
XX
AC AAO73463;
XX
DT 06-MAY-1995 (first entry)
XX
DE Mouse Egr-1 clone OC3.1.
XX
XX Early growth regulatory protein; Egr-1; zinc finger;
XX DNA binding protein; cell growth; transcription;
XX nuclear localization; polynucleotide binding; ss.
XX
XX Mus sp.
OS
XX
FH Key Location/Qualifiers
FT CDS 259..1860
FT /tag= a
FT polyA-signal 1865..1870
FT /tag= b
FT polyA-signal 3053..3058
FT /tag= c
FT polyA-signal 3066..3071
FT /tag= d
XX
PN WO9423030-A.
XX
PD 13-OCT-1994.
XX
PF 10-MAR-1994; 94WO-US02611.
XX
PR 31-MAR-1993; 93US-0040548.
XX
XX (ARCH-) ARCH DEV CORP.
XX
XX Sukhame VP;
XX PI
XX WPI; 1994-333191/41.
XX DR P-PSDB; AAR63129.
XX
XX New early growth regulatory polypeptide and related DNA - useful
XX for modulating transcription, localisation and binding of
XX polynucleotide(s)
XX
XX Disclosure; Page 94-95; 145pp; English.
XX
XX Clone OC3.1 was isolated from a cDNA library derived from
XX BALB/c 3T3 mouse cells, and designated Egr-1. Particular domains of
XX Egr-1 protein have specific functions: activation of transcription
XX (domains given in AAR63131-32), repression of transcription
XX (AAR63133), nuclear localization (AAR63134-35), and polynucleotide
XX binding (AAR63136). Virus and plasmid vectors containing sequences
XX encoding these peptides can be used (by transfection or
XX transformation) to regulate transcription in prokaryotic or
XX eukaryotic hosts.
XX
XX Sequence 3086 BP; 706 A; 939 C; 705 G; 736 T; 0 other;
XX
XX Query Match          100.0%; Score 15; DB 15; Length 3086;
XX Best Local Similarity 100.0%; Pred. No. 2.5e+02;

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BASE COUNT 706 a 939 c 705 g 736 t
 ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 3086;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGGCCGCTGCCAT 15
 ||||||||||||
 DB 273 CTTGGCCGCTGCCAT 259

||||||||||||||
 DB 283 CTTGGCCGCTGCCAT 259

Search completed: December 16, 2002, 13:34:52
 Job time : 3187 secs

RESULT 14

AR014532/c
 LOCUS AR014532 3086 bp DNA linear PAT 05-DEC-1998
 DEFINITION Sequence 15 from patent US 5773583.
 ACCESSION AR014532
 VERSION AR014532.1 GI:3971986
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 UNCLASSIFIED.

REFERENCE 1 (bases 1 to 3086)
 AUTHORS Sukhatme,V.P.
 TITLE Methods and materials relating to the functional domains of DNA
 blinding proteins
 JOURNAL Patent: US 5773583-A 15 30-JUN-1998;
 FEATURES
 source Location/Qualifiers
 1..3086
 /organism="unknown"

BASE COUNT 706 a 939 c 705 g 736 t
 ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 3086;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGGCCGCTGCCAT 15
 ||||||||||||
 DB 273 CTTGGCCGCTGCCAT 259

RESULT 15

AX401867/c
 LOCUS AX401867 3112 bp DNA linear PAT 06-JUN-2002
 DEFINITION Sequence 1543 from Patent W00210453.
 ACCESSION AX401867
 VERSION AX401867.1 GI:21338047
 KEYWORDS
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1
 AUTHORS Mendrick,D., Porter,M.W., Johnson,K.R., Castle,A.L. and
 Elashoff,M.R.
 TITLE Molecular toxicology modeling
 JOURNAL Patent: WO 0210453-A 1543 07-FEB-2002;
 FEATURES
 source Location/Qualifiers
 1..3112
 /organism="Rattus norvegicus"
 /db_xref="taxon:10116"
 /note="EMBL/GenBank Accession No. NM_012551"

BASE COUNT 708 a 951 c 711 g 742 t
 ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 3112;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGGCCGCTGCCAT 15

```

/clone="whyf13f09"
/clone_lib="y" Ogihara unpublished cDNA library, whyf
/tissue_type="spikelet at early flowering"
/dev_stage="feekes" scale 6
/notes="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown under
hydroponic conditions at UC Davis, salt stressed for 12
hours, and for 7 days, then dissected and frozen (Akhunov
in J. Dvorak Lab). Total RNA was prepared from sheath
tissue, equal quantities of RNA were pooled from the two
samples, polyA was purified from the pooled RNA, a cDNA
library was made, and the cDNA clones were in vivo
excised to give Bluescript phagemids in the TJ Clone Lab
at the University of California, Riverside (Akhunov, Chin
, Choi, Close, Fenton, Kianian, Otto, Simons, Zhan).
Plasmid DNA preparations and DNA sequencing were
performed in the OD Anderson Lab (all other authors)."
```

BASE COUNT 74 a 58 c 68 g 50 t 5 others

ORIGIN

Query Match 100.0%; Score 15; DB 13; Length 255;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGGCCGCTGCCAT 15
|||||

DB 208 CTTGGCCGCTGCCAT 194

RESULT 2
BE204615/c 364 bp mRNA linear EST 05-SEP-2000

LOCUS BE204615

DEFINITION EST397291 KVO Medicago truncatula cDNA clone PKV0-1606, mRNA

ACCESSION BE204615

VERSION BE204615.1 GI:8747903

KEYWORDS EST.

SOURCE barrel medic.

ORGANISM Medicago truncatula

TITLE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.

REFERENCE 1 (bases 1 to 364)
Vandenbosch,K., Endre,G., Hur,J., Moore,J., Beremand,P., Ellis,L.,
Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and
Fraser,C.M.
ESTs from uninoculated seedling roots of Medicago truncatula
Unpublished (1999)

JOURNAL Contact: Vandenbosch K

COMMENT Department of Plant Biology
University of Minnesota
220 Bloss Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
Tel: 612 624 2755
Fax: 612 625 1738
Email: kvandenbosch@umn.edu
Texas A&M University name:1264387e
TIGR sequence name:MTGAX51TK
More information is available at:
http://chrysl.tamu.edu/medicago
Seq primer: SKmd (CTA GAA CTA gtc gat cc).

FEATURES

source

1. 364
/organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="PKV0-1606"
/clone_lib="KV0"
/tissue_type="Seedling roots"
/dev_stage="Immediately prior to inoculation with
Sinorhizobium meliloti (0 hour)"
/lab_host="E.coli strain XL0LR"
/notes="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:

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XhoI: cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the unizap XR vector from
stratagene and packaged using gigaPack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XL0LR cells."
```

BASE COUNT 108 a 64 c 92 g 100 t

ORIGIN

Query Match 100.0%; Score 15; DB 10; Length 364;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGGCCGCTGCCAT 15
|||||

DB 275 CTTGGCCGCTGCCAT 261

RESULT 3
BF518720/c 370 bp mRNA linear EST 08-DEC-2000

LOCUS BF518720

DEFINITION EST456171 DSIL Medicago truncatula cDNA clone pDSIL-17D11, mRNA

ACCESSION BF518720

VERSION BF518720.1 GI:11607403

KEYWORDS EST.

SOURCE barrel medic.

ORGANISM Medicago truncatula

TITLE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.

REFERENCE 1 (bases 1 to 370)
Fedorova,M., Pierson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Peng
,H., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S.,
Holt,I.E. and Fraser,C.M.
ESTs from leaves of Medicago truncatula after inoculation with
Colletotrichum trifolii
Unpublished (2000)

JOURNAL Contact: Deborah A. Samac

COMMENT Department of Plant Pathology
University of Minnesota
495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA
Tel: 612 625 1243
Fax: 651 649 5058
Email: debby@puccini.crl.umn.edu
University of Minnesota name: M276140e
TIGR sequence name: MTRBU18TK
More information is available at: http://chrysl.tamu.edu/medicago
Seq primer: SKmd (CTA GAA CTA gtc gat cc).

FEATURES

source

1. 370
/organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pDSIL-17D11"
/clone_lib="DSIL"
/tissue_type="leaves infected with Colletotrichum
trifolii"
/dev_stage="cotyledons and primary leaves harvested 5 and
8 days after inoculation with Colletotrichum trifolii"
/lab_host="E. coli strain XL0LR"
/notes="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA from
cotyledons and primary leaves harvested 5 and 8 days after
inoculation with Colletotrichum trifolii. The cDNA was
directionally ligated into the Uni-ZAP XR vector from
stratagene and packaged using gigaPack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XL0LR cells. Note: EST may
be of fungal origin."

BASE COUNT 106 a 67 c 96 g 100 t 1 others

ORIGIN

Query Match 100.0%; Score 15; DB 12; Length 370;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGGCCGCTGCCAT 15
 |||||||
 DB 275 CTTGGCCGCTGCCAT 261

RESULT 4

AJ503983/c

LOCUS AJ503983 380 bp mRNA linear EST 09-AUG-2002
 DEFINITION AJ503983 MTAMP Medicago truncatula cDNA clone mtgmadcl20040g11,
 mRNA sequence.

ACCESSION AJ503983
 VERSION AJ503983.1 GI:22084911
 KEYWORDS EST.

SOURCE

ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago.

REFERENCE

1 (bases 1 to 380)
 Mantley,K., Bartelsmeier,V., Baler,M.C., Meyer,F., Bartels,D.,
 Bekei,T., Linke,B., Grunwald,U., Franken,P., Kuester,H., Perlick
 ,A.M. and Puehler,A.

TITLE

Detection of transcript sequences from mycorrhizal roots of the
 model mycorrhiza Medicago truncatula genotype A17 - Glomus mosseae
 using the approach of an EST genome project

JOURNAL

COMMENT Unpublished (2002)
 Contact: Kuester H
 Lehrstuhl fuer Genetik
 Universitaet Bielefeld
 Postfach 100131, D-33501 Bielefeld, Germany.

FEATURES

Source

Location/Qualifiers
 1..380
 /organism="Medicago truncatula"
 /db_xref="taxon:3880"
 /clone="mtgmadcl20040g11"
 /clone_1lb="MTAMP"
 /tissue_type="mycorrhizal roots"
 /dev_stage="three weeks"
 /note="Vector: pGEM-T; Site: 1: PstI; Site: 2: SphI;
 genotype A17; cDNA was prepared from polyA+ enriched RNA
 from mycorrhizal roots harvested after three weeks. The
 cDNA was directionally ligated by Medigenomix into the
 pGEM-T vector from Promega using GCATGCCGCCGAGCGCCGACATG
 and CTCGAGCGCCATTATGCGCGG adapters. Plasmids containing
 cDNA inserts were propagated in E. coli DH10b cells."

BASE COUNT

108 a 73 c 97 g 100 t 2 others

ORIGIN

Query Match 100.0%; Score 15; DB 9; Length 380;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGGCCGCTGCCAT 15
 |||||||
 DB 302 CTTGGCCGCTGCCAT 288

RESULT 5

BF116561/c

LOCUS BF116561 386 bp mRNA linear EST 29-DEC-2000
 DEFINITION u90f01.y1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:3666841 5',
 similar to SW:EGRL_MOUSE P08046 EARLY GROWTH RESPONSE PROTEIN 1,;
 mRNA sequence.

ACCESSION BF116561
 VERSION BF116561.1 GI:10986037
 KEYWORDS EST.

SOURCE

ORGANISM

house mouse.
 Mus musculus

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 386)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
imgl.llnl.gov/image/html/lresources.shtml

FEATURES

Source

Location/Qualifiers
 1..386
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:3666841"
 /clone_1lb="NCI_CGAP_Mam6"
 /tissue_type="tumor, gross tissue"
 /dev_stage="7 months"
 /lab_host="DH10B"
 /note="Organ: mammary; Vector: PCMV-SPORT6; Site: 1: SalI;
 Site: 2: NotI; Cloned unidirectionally. Primer: oligo dt.
 library constructed by Life Technologies. Investigators
 providing samples: Lothar Hennighausen/Robin Humphreys,
 NIH"

BASE COUNT 61 a 161 c 104 g 60 t

ORIGIN

Query Match 100.0%; Score 15; DB 12; Length 386;
 Best Local Similarity 100.0%; Pred. No. 2.2e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGGCCGCTGCCAT 15
 |||||||
 DB 265 CTTGGCCGCTGCCAT 251

RESULT 6

AW209329/c

LOCUS AW209329 404 bp mRNA linear EST 03-DEC-1999
 DEFINITION u007f01.y1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:2598841 5',
 similar to gb:M62829 EARLY GROWTH RESPONSE PROTEIN 1 (HUMAN);
 gb:M22326 Mouse growth factor-induced protein (MUSE);, mRNA
 sequence.

ACCESSION AW209329
 VERSION AW209329.1 GI:6515344
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 404)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Other-ESTs: u007f01.x1
 Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Jeffrey Green M.D.
 cDNA Library Preparation: Life Technologies, Inc.

XX 17-NOV-1998.
 PD
 XX 07-APR-1994; 94US-0224482.
 PF
 XX 07-APR-1994; 94US-0224482.
 PR
 XX (ADAM/) ADAMSON E.
 PA (MERC/) MERCOLA D.
 XX
 PI Adamson E, Mercola D;
 DR WPI: 1999-023510/02.
 DR P-PSDB: AAW76984.
 XX
 XX Inhibiting the growth of tumours - using a vector encoding a
 PT mammalian early growth response polypeptide or fragment to inhibit
 PT the mitogenic activity of platelet-derived growth factor
 XX
 PS Disclosure; Fig 2A; 40pp; English.
 XX
 XX This sequence encodes a mouse early growth response protein, Egr-1 which
 CC is used in a method to inhibit the growth of a tumour in a mammal where
 CC the growth is induced by the mitogenic activity of platelet-derived
 CC growth factor, PDGF. The method involves directly administering to the
 CC tumour a retroviral vector comprising an expression control sequence
 CC operatively linked to a nucleic acid sequence encoding a mammalian Egr-1
 CC polypeptide, a nucleic acid sequence encoding a fragment of a mammalian
 CC Egr-1 polypeptide comprising the zinc finger domain or a nucleic acid
 CC sequence that both hybridises to any of the described nucleic acid
 CC sequences, under standard hybridisation conditions, and also encodes a
 CC polypeptide that inhibits the mitogenic activity of PDGF. The methods can
 CC be used for inhibiting the growth of a tumour such as an osteosarcoma, a
 CC fibrosarcoma, a glioblastoma, or a breast carcinoma.
 CC
 SQ Sequence 3068 BP; 688 A; 939 C; 705 G; 736 T; 0 other;
 OY
 Query Match 100.0%; Score 15; DB 20; Length 3068;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 273 CTGGCCGCTGCCAT 15
 273 CTGGCCGCTGCCAT 259
 RESULT 7
 AAA74395/c
 ID AAA74395 standard; cDNA: 3068 BP.
 AC AAA74395;
 XX
 DT 30-NOV-2000 (first entry)
 XX
 DE Mouse Egr-1 coding sequence.
 XX
 XX Mouse; Egr-1; NGF1-A; transcription factor; DNazyme;
 KW vascular smooth muscle cell; post-angioplasty restenosis;
 KW vein graft failure; transplant coronary disease; atherosclerosis;
 KW cerebrovascular infarction; stroke; myocardial; heart attack;
 KW hypertension; peripheral vascular; gangrene; neoplasia; ss.
 XX
 OS Mus sp.
 XX
 PN WO200042173-A1.
 XX
 PD 20-JUL-2000.
 XX
 PF 11-JAN-2000; 2000WO-A000011.
 XX
 PR 11-JAN-1999; 99AU-0008103.
 XX
 PA (UNIX) UNISEARCH LTD.

PA (JOHN) JOHNSON & JOHNSON RES PTY LTD.
 XX
 PI Atkins DG, Baker AR, Khachigian LM;
 XX
 DR WPI: 2000-476054/41.
 XX
 XX DNazyme for treating conditions associated with proliferation or
 PT migration of cells e.g. post-angioplasty restenosis, vein graft failure
 PT and hypertension cleaves mRNA molecules encoding EGR-1 -
 PT
 PS Disclosure; Pages 14-21; 62pp; English.
 XX
 XX The present sequence is mouse Egr-1 (also known as NGF1-A and EGR-1).
 CC Egr-1 is a transcription factor. Egr-1 binds to the promoters of genes
 CC whose products influence cell movement and replication in the artery
 CC wall. DNA-based enzymes (DNazymes), have been developed in the present
 CC invention (see AAA74387-A74394), which can cut Egr-1 mRNA with high
 CC efficiency and specificity, resulting in Egr-1 activity inhibition in
 CC vascular smooth muscle cells. The DNazymes of the present invention can
 CC be used to inhibit EGR-1 activity in cells, inhibit proliferation or
 CC migration of cells and to treat a condition associated with cell
 CC proliferation or migration e.g. post-angioplasty restenosis, vein graft
 CC failure, transplant coronary disease and complications associated with
 CC atherosclerosis e.g. cerebrovascular infarction (stroke), myocardial
 CC infarction (heart attack), hypertension or peripheral vascular disease
 CC e.g. gangrene of the extremities. The cells which are treated are
 CC vascular cells, preferably smooth muscle or endothelial cells or cells
 CC involved in neoplasia.
 CC
 SQ Sequence 3068 BP; 688 A; 939 C; 705 G; 736 T; 0 other;
 OY
 Query Match 100.0%; Score 15; DB 21; Length 3068;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 273 CTGGCCGCTGCCAT 15
 273 CTGGCCGCTGCCAT 259
 RESULT 8
 AAF85130/c
 ID AAF85130 standard; DNA: 3068 BP.
 AC AAF85130;
 XX
 DT 09-JUL-2001 (first entry)
 XX
 DE Nucleotide sequence of murine early growth response factor-1.
 XX
 XX Early growth response factor; EGR; tumour cell; tumour; DNazyme;
 KW antisense oligonucleotide; prostate tumour; hepatocellular carcinoma;
 KW skin carcinoma; breast tumour; ss.
 XX
 OS Mus musculus.
 XX
 PN WO200130394-A1.
 XX
 PD 03-MAY-2001.
 XX
 PF 26-OCT-2000; 2000WO-A001315.
 XX
 PR 26-OCT-1999; 99AU-0003676.
 XX
 PA (UNIX) UNISEARCH LTD.
 XX
 PI Khachigian LM;
 XX
 DR WPI: 2001-300428/31.
 XX
 XX Treating tumors including prostate tumour, breast tumour, skin carcinoma,
 PT comprises administering agent which inhibits induction or decreases
 PT expression of early growth response factor-1 -

JOURNAL Medline 94010293
 MEDLINE 94010293
 PUBMED 7916729

mediates its repressive effect on enhancer function
 Genes Dev. 7 (10), 1966-1978 (1993)

FEATURES
 source Location/Qualifiers
 1.2700
 /organism="Drosophila virilis"
 /db_xref="taxon:7244"

CDS

/codon_start=1
 /product="Hairy-wing protein"
 /protein_id="CA80976.1"
 /db_xref="GI:396677"
 /db_xref="FBI:BASE:FBgn0013144"
 /db_xref="SWISS-PROT:Q08876"
 /translation="MSQEDALPAPPPASSIKISGDKPKREKRTSRMLNDVAK
 AAVASGASVSPRLKPKERTSILKLNNDNDKOTSGDGSVPKPKPAPASRYRT
 SSAPASAVETAKIKTSPSKKKMKHVVQATKSENKAKENTSYVVEDEPTIDPIL
 ADDEVELGAKENGEFVSVGDEDDDDDDDEGGVGGKRRSGNNELKENVEH
 VGGKCTKTRRVKSLKHLKLEFCRYDSGYHLRRADMLKLEKDAVNAEKDISCC
 SESYDFHLGHINCPDCKPSFKTQTSYERHITTHSWSCNDYPCISGNALSGALK
 LHEOQHLRGKFPACKICGDKPMCSYHLCHOKYSANENDMSCKCDRFEYLD
 NCALHKLHGLTOVYKPKPEYHVCNCFYSSTLNIHTRHTGKPEPCDDCDKRES
 ALVALKKHRRYHREKPYCTYCSCSFAYKLYLNRMKHTSERPKNCEKCSFIOA
 TQLRHSTKHLRPYACSLIQKFKTEKQLEHRYKQHTKOKRASFACTECTRSFRISAL
 LKHLHDAGHSVPKSTRARSAKMIERTCAICDKNFDTELRNHRVHEHEDPDPI
 FGTEPPAKRRARKTYVAVAEQLQEQEDQEDVAPRANTAGSLISKTDGNGVVAEEFLD
 EGDGNAQITDLKRRGHLHPLLEGDKATESTAEIDIAESSEKSPVYKKEQKQSL
 AASIAAIADNLEEPSDEFSGEVLEEDLKIENIAKIDLMVLDPOLTKKYGWNS
 SSESVCYKYEKGHDLAKGSAVAYELDYSRMLPTIOLPLFTVYIHNDSIKALLNRP
 DVIIEYVLDEDDDDDEPTDKGRDADNTDITRDVAVESA"

BASE COUNT

743 a 705 c 764 g 488 t

Query Match 100.0%; Score 15; DB 3; Length 2700;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGGCCGCTGCCAT 15
 Db 2229 CTTGGCCGCTGCCAT 2243

RESULT 11

AR058196/c 3068 bp DNA linear PAT 29-SEP-1999
 LOCUS AR058196
 DEFINITION Sequence 1 from patent US 5837692.
 ACCESSION AR058196
 VERSION AR058196.1 GI:5983773
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 3068)
 AUTHORS Mercola,D. and Adamson,E.
 TITLE Inhibition of the mitogenic activity of PDGF by mammalian Egr
 JOURNAL Patent: US 5837692-A 1 17-NOV-1998;
 FEATURES
 source Location/Qualifiers
 1.3068
 /organism="unknown"

BASE COUNT 688 a 939 c 705 g 736 t
 ORIGIN

Query Match 100.0%; Score 15; DB 6; Length 3068;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGGCCGCTGCCAT 15
 Db 273 CTTGGCCGCTGCCAT 259

RESULT 12

MUSEGRIA/c 3068 bp mRNA linear ROD 12-JUN-1993
 LOCUS MUSEGRIA
 DEFINITION Mouse Egr-1 mRNA, complete cds.
 ACCESSION M20157
 VERSION M20157.1 GI:193009
 KEYWORDS Egr-1 gene.
 SOURCE Mouse (strain BALB/c) fibroblast, CDNA to mRNA, clones OC68, OC19L, and OC3.1.
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 3068)
 AUTHORS Sukhatme,V.P., Cao,X., Chang,L.C., Tsai,Morris,C.-H.,
 Stamenkovic,D., Ferreira,P.C.P., Cohen,D.R., Edwards,S.A.,
 Shows,T.B.Jr., Curran,T., Le Beau,M.M. and Adams,E.D.
 TITLE A zinc finger-encoding gene co-regulated with c-fos during growth
 and differentiation, and after cellular depolarization
 JOURNAL Cell 53 (1), 37-43 (1988)
 MEDLINE 88165055
 PUBMED 3127059

Draft entry and computer-readable sequence [1] kindly submitted by
 V.P. Sukhatme 15-NOV-1988

FEATURES
 source Location/Qualifiers
 1.3068
 /organism="Mus musculus"
 /db_xref="taxon:10090"

mRNA

/product="Egr-1 mRNA"
 259..1860
 /note="Egr-1 protein"
 /codon_start=1
 /protein_id="AA37544.1"
 /db_xref="GI:309213"

BASE COUNT 688 a 939 c 705 g 736 t
 ORIGIN Unreported.

Query Match 100.0%; Score 15; DB 10; Length 3068;
 Best Local Similarity 100.0%; Pred. No. 2.1e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGGCCGCTGCCAT 15
 Db 273 CTTGGCCGCTGCCAT 259

RESULT 13
 AR012093/c 3066 bp DNA linear PAT 04-DEC-1998
 LOCUS AR012093
 DEFINITION Sequence 15 from patent US 5763209.
 ACCESSION AR012093
 VERSION AR012093.1 GI:3970083
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 3066)
 AUTHORS Sukhatme,V.P.
 TITLE Methods and materials relating to the functional domains of DNA
 binding proteins
 JOURNAL Patent: US 5763209-A 15 09-JUN-1998;
 FEATURES
 source Location/Qualifiers
 1.3086
 /organism="unknown"

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGCCCGCTGCCAT 15
 |||||||
 DB 273 CTTGCCCGCTGCCAT 259

RESULT 11
 ABR63636/C
 ID ABR63636 standard; cDNA; 3112 BP.
 AC ABR63636;
 DT 18-JUN-2002 (first entry)
 DE Rat sequence differentially expressed in response to a hepatotoxin #1543.
 KW Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening;
 KW differential expression; centrilobular necrosis; steatosis.
 OS Rattus norvegicus.
 PN W0200210453-A2.
 PD 07-FEB-2002.
 PF 30-JUL-2001; 2001WO-US23872.
 PR 31-JUL-2000; 2000US-222040P.
 PR 02-NOV-2000; 2000US-244880P.
 PR 11-MAY-2001; 2001US-290023P.
 PR 15-MAY-2001; 2001US-290645P.
 PR 22-MAY-2001; 2001US-292336P.
 PR 06-JUN-2001; 2001US-295798P.
 PR 13-JUN-2001; 2001US-297457P.
 PR 19-JUN-2001; 2001US-298884P.
 PR 09-JUL-2001; 2001US-303459P.
 XX (GENE-) GENE LOGIC INC.
 PI Mendrick D, Porter MW, Johnson KR, Castle AL, Elashoff MR;
 DR WPI: 2002-241625/29.
 XX
 PT Predicting toxic effects of compounds or the progression of these toxic
 PT effects by determining the changes in gene expression in tissues or
 PT cells exposed to the toxin and comparing these to gene expression in
 PT unexposed tissues or cells -
 PS
 PS Claim 1; Seq ID No 1543; 2399P; English.
 XX
 XX The invention relates to methods for predicting toxic effects of
 CC compounds or the progression of these toxic effects by determining the
 CC global changes in gene expression in tissues or cells exposed to the
 CC toxin and comparing these to gene expression in unexposed tissues or
 CC cells. Also included are methods of predicting at least one toxic
 CC effect of a compound or progression of a toxic effect, preferably the
 CC hepatotoxicity of a compound, comprising detecting the level of
 CC expression in a tissue or cell sample exposed to the compound of two or
 CC more genes listed in the specification, where differential expression of
 CC the genes is indicative of at least one toxic effect or progression.
 CC The method can also be used to identify an agent which modulates the
 CC toxic response and predict cellular pathways that a compound modulates
 CC in a cell. The methods utilize a set of at least two probes (on a solid
 CC support in kit form), where each of the probes comprises a sequence that
 CC specifically hybridises to a gene listed in the specification, a computer
 CC system comprising a database containing information identifying the
 CC expression level in a tissue or cell sample exposed to a hepatotoxin of a
 CC set of genes comprising at least two genes listed in the specification,
 CC and a user interface to view the information used to present information
 CC identifying the expression level in a tissue or cell of at least one gene
 CC listed in the specification. The method is useful for elucidating global
 CC changes in gene expression and for identifying toxicity markers in

CC tissues or cell exposed to a known toxin. The genes may be used as
 CC toxicity markers in drug screening and toxicity assays. The genes and
 CC gene expression information may be used as diagnostic markers for the
 CC prediction or identification of the physiological state of tissue or cell
 CC sample that has been exposed to a compound or agent. Hepatotoxicity
 CC is characterised by centrilobular necrosis and steatosis. The present
 CC sequence is an expressed sequence tag (EST) or cDNA derived from a gene
 CC which is differentially expressed in response to a hepatotoxic agent.
 CC
 SO Sequence 3112 BP; 708 A; 951 C; 711 G; 742 T; 0 other.

Query Match 100.0%; Score 15; DB 24; Length 3112;
 Best Local Similarity 100.0%; Pred. No. 2.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTTGCCCGCTGCCAT 15
 |||||||
 DB 283 CTTGCCCGCTGCCAT 269

RESULT 12
 AAA74396/C
 ID AAA74396 standard; cDNA; 4321 BP.
 AC AAA74396;
 DT 30-NOV-2000 (first entry)
 DE Rat Egr-1 coding sequence.
 XX
 XX Rat; Egr-1; NGF1-A; transcription factor; DNzyme;
 KW vascular smooth muscle cell; post-angioplasty restenosis;
 KW vein graft failure; transplant coronary disease; atherosclerosis;
 KW cerebrovascular infarction; stroke; myocardial; heart attack;
 KW hypertension; peripheral vascular; gangrene; neoplasia; ss.
 XX
 OS Rattus sp.
 PN W0200042173-A1.
 PD 20-JUL-2000.
 PF 11-JAN-2000; 2000WO-A000011.
 PR 11-JAN-1999; 99AU-0008103.
 PR (UNIT) UNISEARCH LTD.
 PA (JOHN) JOHNSON & JOHNSON RES PTY LTD.
 PI Atkins DG, Baker AR, Khachigian LM;
 DR WPI: 2000-476054/41.
 XX
 XX DNzyme for treating conditions associated with proliferation or
 PT migration of cells, e.g. post-angioplasty restenosis, vein graft failure
 PT and hypertension cleaves mRNA molecules encoding EGR-1 -
 PT
 PS Disclosure: Pages 14-21; 62pp; English.
 XX
 XX The present sequence is rat Egr-1 (also known as NGF1-A and EGR-1).
 CC Egr-1 is a transcription factor. Egr-1 binds to the promoters of genes
 CC whose products influence cell movement and replication in the artery
 CC wall. DNA-based enzymes (DNzymes), have been developed in the present
 CC invention (see AAA74387-A74394), which can cut Egr-1 mRNA with high
 CC efficiency and specificity, resulting in Egr-1 activity inhibition in
 CC vascular smooth muscle cells. The DNzymes of the present invention can
 CC be used to inhibit EGR-1 activity in cells, inhibit proliferation or
 CC migration of cells and to treat a condition associated with cell
 CC proliferation or migration e.g. post-angioplasty restenosis, vein graft
 CC failure, transplant coronary disease and complications associated with
 CC atherosclerosis e.g. cerebrovascular infarction (stroke), myocardial
 CC infarction (heart attack), hypertension or peripheral vascular disease
 CC e.g. gangrene of the extremities. The cells which are treated are

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OM nucleic - nucleic search, using sw model

Run on: December 16, 2002, 11:13:08 ; Search time 3183 Seconds

(without alignments)
137.148 Million cell updates/sec

Title: US-09-648-389a-1

Perfect score: 15

Sequence: 1 cttgcgcgcgcgcac 15

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: gb_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlg_mus:*
34: em_hlg_pin:*
35: em_hlg_rod:*
36: em_hlg_mam:*
37: em_hlg_vrt:*
38: em_sy:*
39: em_hlggo_hum:*
40: em_hlggo_mus:*
41: em_hlggo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	15	100.0	390	10	MUSKROX24A	M38174 Mouse nucle
2	15	100.0	676	10	RNKROX1	U75398 Rattus norv
3	15	100.0	843	6	AR012087	AR012087 Sequence
4	15	100.0	843	6	AR014526	AR014526 Sequence
5	15	100.0	933	8	CAR6024	AJ006024 Cicer ari
6	15	100.0	1980	14	AC2NK24	M18041 Avian trans
7	15	100.0	1983	10	MUSKROX251	M28844 Mus muscu
8	15	100.0	2253	5	CHKCFOSA	M37000 Chicken c-f
9	15	100.0	2253	5	GDPOS	Y00659 Chicken fos
10	15	100.0	2700	3	DVHRYMCA	225520 D.villilis H
11	15	100.0	3068	6	AR058196	AR058196 Sequence
12	15	100.0	3068	10	MUSEGRIA	M20157 Mouse Egr-1
13	15	100.0	3086	6	AR012093	AR012093 Sequence
14	15	100.0	3086	6	AR014532	AR014532 Sequence
15	15	100.0	3112	6	AX401867	AX401867 Sequence
16	15	100.0	3112	10	RATNGF1A	M18416 Rat nerve g
17	15	100.0	3858	5	CHKCFOS	M18043 Chicken c-f
18	15	100.0	4321	10	RATNGF1A	J04154 Rattus norv
19	15	100.0	4494	6	AX306251	AX306251 Sequence
20	15	100.0	4494	10	MUSTPEZIF	M22326 Mouse growt
21	15	100.0	10528	1	AE009847	AE009847 Pyrodacul
22	15	100.0	38343	3	CEP21D9	281510 Caenorhabdi
23	15	100.0	56870	2	CEY39B6_3	Continuation (4 of
24	15	100.0	59907	2	AC130689	AC130689 Homo sapi
25	15	100.0	71503	2	AC129488	AC129488 Homo sapi
26	15	100.0	71503	2	AC129488	AC129488 Homo sapi
27	15	100.0	127304	2	AC119051	AC119051 Gallus ga
28	15	100.0	140053	2	AC007873	AC007873 Homo sapi
29	15	100.0	153695	2	CNS08CAL	AL831808 Oryza sat
30	15	100.0	153824	2	AC118806	AC118806 Rattus no
31	15	100.0	166138	2	AC099684	AC099684 Homo sapi
32	15	100.0	175131	2	AC114820	AC114820 Mus muscu
33	15	100.0	190875	2	AC022255	AC022255 Homo sapi
34	15	100.0	208395	2	AC098450	AC098450 Rattus no
35	15	100.0	212696	2	AL772410	AL772410 Mus muscu
36	15	100.0	212696	2	AL772410	X88786 Porceto viru
37	14	93.3	708	14	PVXCPSW2	M34453 S.mansoni 2
38	14	93.3	1058	38	SCMIMP23A	BC022626 Mus muscu
39	14	93.3	1434	10	BC022626	X57478 S.cerevisia
40	14	93.3	1606	9	SCMTR1	AL833144 Homo sapi
41	14	93.3	1873	9	HSW804455	AF176328 Mus muscu
42	14	93.3	1922	10	AF176328	BC010694 Mus muscu
43	14	93.3	1938	10	BC010694	217317 Kluyveromyc
44	14	93.3	1961	8	KLTRANAL	BC029146 Homo sapi
45	14	93.3	2100	6	AX121824	AX121824 Sequence

ALIGNMENTS

RESULT 1
MUSKROX24A/c 390 bp mRNA linear ROD 27-APR-1993
LOCUS MUSKROX24A
DEFINITION Mouse nuclear protein Krox-24 mRNA, 5' end.
ACCESSION M38174
VERSION M38174.1 GI:198606
KEYWORDS nuclear protein; transcriptional activator.
SOURCE Mouse, CDNA to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 390)
Lemaire,P., Vesque,C., Schmitt,J., Stunnenberg,H., Frank,R. and
Charney,P.
The serum-inducible mouse gene Krox-24 encodes a sequence-specific

Db 15 CTTGGCCGCTGCCAT 1

RESULT 5
LOCUS CAR6024 953 bp mRNA linear PLN 11-MAY-1998
DEFINITION Cicer arletinum mRNA for cysteine synthase, partial.
ACCESSION AJ006024
VERSION AJ006024.1 GI:3127889
KEYWORDS cysteine synthase.
SOURCE chickpea.
ORGANISM Cicer arletinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Ciceraceae; Cicer.
REFERENCE 1 (bases 1 to 953)
AUTHORS Labrador, E.
TITLE Direct Submission
JOURNAL Submitted (04-MAY-1998) Labrador E., Dpto. Fisiologia Vegetal, Univ. Salamanca, Campus Miguel de Unamuno, Pza. Doctores de la Reina s/n, 37007-Salamanca, SPAIN
REFERENCE 2 (bases 1 to 953)
AUTHORS Dopico, B., Esteban, R. and Labrador, E.
TITLE CDNA expressed in chickpea epicotyls
JOURNAL Unpublished
FEATURES
source Location/Qualifiers
1..953
/organism="Cicer arletinum"
/cultivar="Castellana"
/db_xref="taxon:3827"
/clone="Cancys"
/tissue_type="etiolated epicotyls"
/dev_stage="5 day old seedlings"
<1..803
/EC_number="4.2.99.8"
/codon_start=3
/product="cysteine synthase, O-acetyl-L-serine (thiol)-lyase"
/protein_id="CAA06819.1"
/db_xref="GI:3127890"
/db_xref="SPTREMBL:065747"
/translation="AEKGIITPGOSVLEPTSGWTGIGLAFAAAKGYKILITPAS MSLEKRIILFAGALVLDPAKGGKGAQAEEILATPNAYIILQEPNPAPVHY ETTGEIKGTGKVDVSGITGEGITGAGKYEONPNKIVGVPVPSVLSGG KPGHKIGIGAGFVGLVLEVLIDEVLIQSSDEAIEFAKILALEGFLVGISSGAAA AAATKIRAPENAGKLIIVFPSEFERYLSVLFESVRAQETMTFEP"
BASE COUNT 288 a 169 c 229 g 267 t
ORIGIN

Query Match 100.0%; Score 15; DB 8; Length 953;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGGCCGCTGCCAT 15
|||||
Db 101 CTTGGCCGCTGCCAT 87

RESULT 6
LOCUS AC2NK24 1980 bp ss-RNA linear VRL 10-MAY-1995
DEFINITION Avian transforming proviral retrovirus NK24 v-fos gene, partial cds.
ACCESSION M18041
VERSION M18041.1 GI:209654
KEYWORDS c-myc proto-oncogene; fos gene.
SOURCE Avian transforming proviral retrovirus NK24 RNA, from a chicken nephroblastoma, passed in quail embryo fibroblast (QEF) cells, clone 2401.
ORGANISM Avian carcinoma virus
VIRUSES: Retroviral viruses; Retroviridae; Alpharetrovirus.
REFERENCE 1 (bases 1 to 1980)

AUTHORS Nishizawa, M., Goto, N. and Kawai, S.
TITLE An avian transforming retrovirus isolated from a nephroblastoma that carries the fos gene as the oncogene
JOURNAL J. Virol. 61 (12), 3733-3740 (1987)
MEDLINE 88062920
PUBMED 2824811
COMMENT Printed copy of sequence for [1] kindly provided by S. Kawai, 15-MAR-1988.

FEATURES
source Location/Qualifiers
1..1980
/organism="Avian carcinoma virus"
/db_xref="taxon:11958"
<1..1098
/codon_start=1
/product="gag/NK24 fusion protein"
/protein_id="AAA66158.1"
/db_xref="GI:209655"
/translation="SDLSPTARAPYIIOCFRQKSQPDIOQLRAAPSTITPGEIINS QDFCTDLAVSSANFPTVTAISTPDLQVLPSTLISSVAPSONGHPYGPAPAPA AYSRAVLAKAPGSGQSIGRRGVQLSPSEERKRIIRERNKMAAKRNRRRELT DLOAETDLEERKSAIOAEIANLKEKLEIEILAAHRPACMKPELRFSEELAAATA LDIGAPSPAAAEAPALPIMTPEAPVAPPKPEPSGGLKELAPPELRFSEAPREASR SVPMDDLPGASSFVASDMPKIGAGSGGELEPCFTVVTCTPCPSYTTSTFTYTPPAD APESCAAHRRGSSSNPSSDSLSPTLIAT"
128..129
/organism="Avian carcinoma virus"
1200..1201
/organism="Avian carcinoma virus"
1255..1256
/organism="Avian carcinoma virus"
1718..>1980
/note="The first start codon in the ORF is located at position 1718; putative"
/codon_start=1
/product="glycoprotein 85"
/protein_id="AAA66159.1"
/db_xref="GI:806277"
/translation="WMDEPQLQLGSOSLPNITVTOIPGAVAGCIGFTPGSPAGV YGMGRGELTHILINPDPNPFNRASNSTEPTVTYADRHNLF"
BASE COUNT 380 a 667 c 573 g 360 t
ORIGIN 3 bp upstream of BglII.

Query Match 100.0%; Score 15; DB 14; Length 1980;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGGCCGCTGCCAT 15
|||||
Db 450 CTTGGCCGCTGCCAT 436

RESULT 7
LOCUS MUSKROX2S1 1983 bp DNA linear ROD 21-MAY-1996
DEFINITION Mus musculus zinc finger protein (Krox-24) gene, exon 1.
ACCESSION M28844
VERSION M28844.1 GI:342026
KEYWORDS DNA-binding protein; zinc finger protein.
SEGMENT 1 of 2
SOURCE Mus musculus DNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1983)
AUTHORS Janssen-Timmen, U., Lemaire, P., Mattel, M.G., Revelant, O. and Charnay, P.
TITLE Structure, chromosome mapping and regulation of the mouse zinc-finger gene Krox-24; evidence for a common regulatory pathway for immediate-early serum-response genes
JOURNAL Gene 80 (2), 325-336 (1989)
MEDLINE 90060781
PUBMED 2511075
FEATURES
Location/Qualifiers

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Washington University Genome Sequencing Center
 cDNA distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
www-bio.linn.gov/bdrip/image/image.html

MG1:1022301

Seq primer: -40RP from Gldco
 High quality sequence stop: 205.

FEATURES

SOURCE

1. 404

/organism="Mus musculus"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone_image="238841"

/clone_lib="NCI_CGAP_Man6"

/sex="female, virgin"

/tissue_type="infiltrating ductal carcinoma"

/dev_stage="5 months"

/lab_host="DH10B"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site: 1; Salt: 1; Site: 2; NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"

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/origin="61 a 168 c 111 g 63 t 1 others"

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/db="251 CTTGGCCGCTGCCAT 237"

/result="7"

/locus="AL373362/c"

/definition="MBA57D03F1 MBA Medicago truncatula cDNA clone MBA57D03 F3, mRNA sequence."

/accession="AL373362"

/version="AL373362.1"

/keywords="GI:9673115"

/source="EST. barrel medic."

/organism="Medicago truncatula"

/eukaryota="Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago. 1 (bases 1 to 409)"

/journal="Journet,E.P., Crespeau,H., van Tuinen,D., Gouzy,J., Jallou,O., Niebel,A., Carreau,Y., Chataigner,O., Kahn,D., Gianfranceschi-Pearson, V. and Gamas,P."

/comment="Medicago truncatula ESTs from nitrogen-starved roots"

/unpublished="(2000)"

/contact="Genoscope"

/genoscope="Centre National de Sequencage"

/bp="191 91006 EVRY cedex - France"

/email="segref@genoscope.cns.fr, Web: www.genoscope.cns.fr"

/contact="Pascal Gamas and Etienne-Pascal Journet, Laboratoire de Biologie Moleculaire des Relations Microorganismes, CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email: Mt-est@toulouse.inra.fr Website: http://sequence.toulouse.inra.fr/Mtruncatula.html). Location/Qualifiers"

1. 409

/organism="Medicago truncatula"

/cultivar="Jemalong"

/db_xref="taxon:3880"

/clone="MBA57D03"

/clone_lib="MBA"

/tissue_type="root tips"

/dev_stage="harvested after 3 days of N-starvation"

/note="Vector: pBluescript PSK; Site: 1; EcoRI; Site: 2; XhoI; Plants were grown in an aeroponic chamber for 14 days on nitrogen-rich medium followed by 3 days on N-free medium. RNA was extracted from root tips (1-3 cm). cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into Uni-ZAPXR vector from Stratagene and packaged using Gigapack Gold packaging extracts. Plasmids containing cDNA inserts were mass-excisised from phage stocks using ExSact helper phage and propagated in SDR cells. Clone ordering and sequencing was performed by the Centre National de Sequencage (Genoscope, Evry, France)."

/base_count="127 a 83 c 100 g 99 t"

/origin="127 a 83 c 100 g 99 t"

/query_match="100.0%; Score 15; DB 9; Length 409; Best Local Similarity 100.0%; Pred. No. 2.2e+03; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;"

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/db="90 CTTGGCCGCTGCCAT 76"

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/accession="BF519247"

/version="BF519247.1"

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/source="EST. barrel medic."

/organism="Medicago truncatula"

/eukaryota="Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago. 1 (bases 1 to 418)"

/journal="Fedorova,M., Peterson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Peng, H., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.M."

/comment="ESTs from leaves of Medicago truncatula after inoculation with Colletotrichum trifolii"

/unpublished="(2000)"

/contact="Deborah A. Samac"

/department="Department of Plant Pathology"

/university="University of Minnesota"

/address="495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA"

/tel="Tel: 612 625 1243"

/fax="Fax: 651 649 5058"

/email="debby@puchat.crl.umn.edu"

/university="University of Minnesota"

/tiger="TIGR sequence name: MTFCE65TX"

/more="More information is available at: http://chryslie.tamu.edu/medicago"

/seg="Seg primer: SKmod (CTA GAA GTG gAT CC). Location/Qualifiers"

1. 418

/organism="Medicago truncatula"

/cultivar="genotype A17"

/db_xref="taxon:3880"

/clone="pDSIL-20K9"

/clone_lib="DSIL"

/tissue_type="leaves infected with Colletotrichum trifolii"

/dev_stage="cotyledons and primary leaves harvested 5 and 8 days after inoculation with Colletotrichum trifolii"

/lab_host="E. coli strain XL0LR"

/note="Vector: pBluescript SK-; Site: 1; EcoRI; Site: 2; XhoI; cDNA was prepared from polyA+ enriched RNA from cotyledons and primary leaves harvested 5 and 8 days after inoculation with Colletotrichum trifolii. The cDNA was"

/base_count="100.0%; Score 15; DB 9; Length 409; Best Local Similarity 100.0%; Pred. No. 2.2e+03; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;"

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/keywords="GI:11607930"

/source="EST. barrel medic."

/organism="Medicago truncatula"

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/journal="Fedorova,M., Peterson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Peng, H., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.M."

/comment="ESTs from leaves of Medicago truncatula after inoculation with Colletotrichum trifolii"

/unpublished="(2000)"

/contact="Deborah A. Samac"

/department="Department of Plant Pathology"

/university="University of Minnesota"

/address="495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA"

/tel="Tel: 612 625 1243"

/fax="Fax: 651 649 5058"

/email="debby@puchat.crl.umn.edu"

/university="University of Minnesota"

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1. 418

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/tissue_type="leaves infected with Colletotrichum trifolii"

/dev_stage="cotyledons and primary leaves harvested 5 and 8 days after inoculation with Colletotrichum trifolii"

/lab_host="E. coli strain XL0LR"

/note="Vector: pBluescript SK-; Site: 1; EcoRI; Site: 2; XhoI; cDNA was prepared from polyA+ enriched RNA from cotyledons and primary leaves harvested 5 and 8 days after inoculation with Colletotrichum trifolii. The cDNA was"

/base_count="100.0%; Score 15; DB 9; Length 409; Best Local Similarity 100.0%; Pred. No. 2.2e+03; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;"

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/journal="Fedorova,M., Peterson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Peng, H., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.M."

/comment="ESTs from leaves of Medicago truncatula after inoculation with Colletotrichum trifolii"

/unpublished="(2000)"

/contact="Deborah A. Samac"

/department="Department of Plant Pathology"

/university="University of Minnesota"

/address="495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA"

/tel="Tel: 612 625 1243"

/fax="Fax: 651 649 5058"

/email="debby@puchat.crl.umn.edu"

/university="University of Minnesota"

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/more="More information is available at: http://chryslie.tamu.edu/medicago"

/seg="Seg primer: SKmod (CTA GAA GTG gAT CC). Location/Qualifiers"

1. 418

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/cultivar="genotype A17"

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/clone_lib="DSIL"

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/dev_stage="cotyledons and primary leaves harvested 5 and 8 days after inoculation with Colletotrichum trifolii"

/lab_host="E. coli strain XL0LR"

/note="Vector: pBluescript SK-; Site: 1; EcoRI; Site: 2; XhoI; cDNA was prepared from polyA+ enriched RNA from cotyledons and primary leaves harvested 5 and 8 days after inoculation with Colletotrichum trifolii. The cDNA was"

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/journal="Fedorova,M., Peterson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Peng, H., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.M."

/comment="ESTs from leaves of Medicago truncatula after inoculation with Colletotrichum trifolii"

/unpublished="(2000)"

/contact="Deborah A. Samac"

/department="Department of Plant Pathology"

/university="University of Minnesota"

/address="495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA"

/tel="Tel: 612 625 1243"

/fax="Fax: 651 649 5058"

/email="debby@puchat.crl.umn.edu"

/university="University of Minnesota"

/tiger="TIGR sequence name: MTFCE65TX"

/more="More information is available at: http://chryslie.tamu.edu/medicago"

/seg="Seg primer: SKmod (CTA GAA GTG gAT CC). Location/Qualifiers"

1. 418

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/cultivar="genotype A17"

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/clone_lib="DSIL"

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/dev_stage="cotyledons and primary leaves harvested 5 and 8 days after inoculation with Colletotrichum trifolii"

/lab_host="E. coli strain XL0LR"

/note="Vector: pBluescript SK-; Site: 1; EcoRI; Site: 2; XhoI; cDNA was prepared from polyA+ enriched RNA from cotyledons and primary leaves harvested 5 and 8 days after inoculation with Colletotrichum trifolii. The cDNA was"

/base_count="100.0%; Score 15; DB 9; Length 409; Best Local Similarity 100.0%; Pred. No. 2.2e+03; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;"

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/version="BF519247.1"

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/source="EST. barrel medic."

/organism="Medicago truncatula"

/eukaryota="Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago. 1 (bases 1 to 418)"

/journal="Fedorova,M., Peterson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Peng, H., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.M."

ACCESSION AM207985
 VERSION AM207985.2 GI:7773205
 KEYWORDS EST.
 SOURCE barrel medic.
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
 Medicago.
 REFERENCE 1 (bases 1 to 429)
 AUTHORS Fedorova,M., Plesion,B.L., Samac,D.A., Gantt,J.S., Vance,C.P.,
 Gonzales,M.B. and Ellis,L.
 TITLE ESTs from Medicago truncatula roots infected with Phytophthora
 medicaginis
 JOURNAL Unpublished (2000)
 COMMENT On Dec 2, 1999 this sequence version replaced gi:6507422.
 Contact: Carroll P. Vance
 Department of Agronomy and Plant Genetics
 University of Minnesota
 411 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108 USA
 Tel: 612 625 5715
 Fax: 651-649-5058
 Email: vance004@maroon.tc.umn.edu
 Date: 9/28/99; Updated to the Database of Expressed Sequence Tags
 (dbEST) on 04/27/00; More information is available at
 'http://chryste.tamu.edu/medicago'.
 Seq primer: r3.
 FEATURES
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 /cultivar="genotype A17"
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 /clone_lib="DSIR"
 /tissue_type="roots infected with Phytophthora
 medicaginis"
 /dev_stage="roots harvested at 10 days post inoculation
 with Phytophthora medicaginis"
 /lab_host="E. coli strain XLOLR"
 /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
 XhoI; cDNA was prepared from polyA+ enriched RNA from
 roots harvested at 10 days post inoculation with
 Phytophthora medicaginis. The cDNA was directionally
 ligated into the uni-ZAP XR vector from Stratagene and
 packaged using GigaPack III Gold packaging extracts.
 Plasmids containing cDNA inserts were excised from the
 recombinant lambda-ZAP phage using Ex-Assist helper phage
 and propagated in XLOLR cells. Note: EST may be of fungal
 origin."
 BASE COUNT 126 a 82 c 105 g 116 t
 ORIGIN
 Query Match 100.0%; Score 15; DB 10; Length 429;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTGGCCGCTGCCAT 15
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 Db 350 CTTGGCCGCTGCCAT 336
 RESULT 12
 AM127154/c 438 bp mRNA linear EST 07-SEP-2000
 LOCUS
 DEFINITION M110088 GVN Medicago truncatula cDNA clone N10, mRNA sequence.
 ACCESSION AM127154
 VERSION AM127154.2 GI:7771071
 KEYWORDS EST.
 SOURCE barrel medic.
 ORGANISM Medicago truncatula
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;

Medicago.
 REFERENCE 1 (bases 1 to 438)
 AUTHORS Fedorova,M., Plesion,B.L., Samac,D.A., Gantt,J.S., Vance,C.P.,
 Gonzales,M.B. and Ellis,L.
 TITLE ESTs from effective root nodules of Medicago truncatula
 JOURNAL Unpublished (2000)
 COMMENT On Oct 25, 1999 this sequence version replaced gi:6115058.
 Contact: Carroll P. Vance
 Department of Agronomy and Plant Genetics
 University of Minnesota
 411 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108 USA
 Tel: 612 625 5715
 Fax: 651-649-5058
 Email: vance004@maroon.tc.umn.edu
 Date: 9/8/99; Updated to the Database of Expressed Sequence Tags
 (dbEST) on 04/27/00; More information is available at
 'http://chryste.tamu.edu/medicago'.
 Seq primer: r3.
 FEATURES
 source
 Location/Qualifiers
 1..438
 /organism="Medicago truncatula"
 /cultivar="genotype A17"
 /db_xref="taxon:3880"
 /clone="N10"
 /clone_lib="GVN"
 /tissue_type="N2-fixing root nodules"
 /dev_stage="effective root nodules harvested one month
 post inoculation with Sinorhizobium meliloti"
 /lab_host="E. coli strain XLOLR"
 /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
 XhoI; cDNA was prepared from polyA+ enriched RNA from
 effective root nodules harvested one month post
 inoculation with Sinorhizobium meliloti. The cDNA was
 directionally ligated into the Uni-ZAP XR vector from
 Stratagene and packaged using GigaPack III Gold packaging
 extracts. Plasmids containing cDNA inserts were excised
 from the recombinant lambda-ZAP phage using Ex-Assist
 helper phage and propagated in XLOLR cells."
 BASE COUNT 136 a 87 c 112 g 103 t
 ORIGIN
 Query Match 100.0%; Score 15; DB 10; Length 438;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTGGCCGCTGCCAT 15
 ||||||||||||||||
 Db 117 CTTGGCCGCTGCCAT 103
 RESULT 13
 AW321427/c 443 bp mRNA linear EST 25-JAN-2000
 LOCUS
 DEFINITION uc031f11.y1 NCI-CGAP Mam4 Mus musculus cDNA clone IMAGE:2631117 5
 similar to gb:M20157 Mouse Egr-1 mRNA, complete cds (MOUSE);, mRNA
 sequence.
 ACCESSION AW321427
 VERSION AW321427.1 GI:6750971
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 443)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaaps-r@mail.nih.gov
 Tissue Procurement: Jeffrey Green M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed By: The I.M.A.G.E. Consortium (ILNLT)

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 16, 2002, 11:13:18 ; Search time 2423 Seconds

(without alignments)
100.261 Million cell updates/sec

Title: US-09-648-389A-1

Perfect score: 15
Sequence: 1 cttgcccgcgtgccat 15

Scoring table: IDENTITY_NUC
Gapop 10.0 / Gapext 1.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_estlm:*
3: em_estln:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vit:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	255	13	BJ320065
2	15	100.0	364	10	BE204615
3	15	100.0	370	12	BF518720
4	15	100.0	380	9	AJ503983
5	15	100.0	386	12	BF116561
6	15	100.0	404	10	AM209329

Result No.	Score	Query Match	Length	ID	Description
7	15	100.0	409	9	AL373362
8	15	100.0	418	12	BF519247
9	15	100.0	421	14	BQ140289
10	15	100.0	426	10	AM911108
11	15	100.0	429	10	AM207985
12	15	100.0	438	10	AM127154
13	15	100.0	443	10	AM321427
14	15	100.0	451	13	BI72170
15	15	100.0	459	13	BB662529
16	15	100.0	469	9	AJ503524
17	15	100.0	476	12	BF454382
18	15	100.0	477	9	AL381682
19	15	100.0	481	12	BG448249
20	15	100.0	490	10	BE203104
21	15	100.0	498	10	BE203605
22	15	100.0	510	12	BF520604
23	15	100.0	514	10	AM559351
24	15	100.0	520	12	BF634953
25	15	100.0	523	12	BF645970
26	15	100.0	542	12	BF320644
27	15	100.0	583	17	BH084990
28	15	100.0	612	12	BG448073
29	15	100.0	620	10	BB631108
30	15	100.0	623	10	AM775920
31	15	100.0	627	12	BF005244
32	15	100.0	631	10	BB636948
33	15	100.0	632	10	BE317448
34	15	100.0	637	10	AM775304
35	15	100.0	644	10	AM776844
36	15	100.0	651	13	BJ314563
37	15	100.0	651	13	BJ314563
38	15	100.0	653	12	BG451772
39	15	100.0	655	12	BF520599
40	15	100.0	655	13	BT309270
41	15	100.0	658	13	BT264457
42	15	100.0	659	14	BQ139038
43	15	100.0	660	12	BG586431
44	15	100.0	662	10	AM694259
45	15	100.0	662	12	BG452657

ALIGNMENTS

RESULT 1
BJ320065/c 255 bp mRNA linear EST 09-APR-2002

LOCUS BJ320065 Y. Ogihara unpublished cDNA library, wh_yf Triticum
DEFINITION aestivum cDNA clone wh_yf13f09 3', mRNA sequence.

ACCESSION BJ320065
VERSION BJ320065.1 GI:20123819
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum

REFERENCE 1 (bases 1 to 255)
Ogihara, Y. and Murai, K.
Expressed genes in Triticum aestivum
Unpublished (2002)
CONTACT: Tadasu Shin-1
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin1@genes.nig.ac.jp

FEATURES
Source
1..255
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"

PR reducing incidence of restenosis
 XX
 PS Claim 11; Page 22; 29pp; English.
 XX
 CC This sequence represents an antisense oligonucleotide directed against
 CC rat Egr-1 (an early growth response gene product) that can be used in the
 CC method of the invention. The method is for inhibiting the proliferation
 CC of cells, and comprises inhibiting induction or decreasing expression of
 CC Egr-1, or decreasing the nuclear accumulation or activity of the Egr-1
 CC gene product. The method can be used to inhibit proliferation of cells,
 CC migration of cells to sites of injury and remodelling of vascular wall
 CC associated with atherosclerosis or restenosis and especially to reduce
 CC the incidence of restenosis by administration of an agent effective in
 CC the method.
 XX
 SQ Sequence 15 BP; 1 A; 6 C; 4 G; 4 T; 0 other;
 Query Match 100.0%; Score 15; DB 18; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTGGCCGCTGCCAT 15
 DB 1 CTTGGCCGCTGCCAT 15
 RESULT 2
 AAA74448
 ID AAA74448 standard; DNA; 15 BP.
 AC AAA74448;
 XX
 DT 30-NOV-2000 (first entry)
 XX
 DE Rat AS2 sequence.
 XX
 KM Rat; Egr-1; NGFI-A; transcription factor; DNazyme;
 KM vascular smooth muscle cell; post-angioplasty restenosis;
 KM vein graft failure; transplant coronary disease; atherosclerosis;
 KM cerebrovascular infarction; stroke; myocardial; heart attack;
 KM hypertension; peripheral vascular; gangrene; neoplasia; ss.
 XX
 OS Rattus sp.
 XX
 PN WO200042173-A1.
 XX
 PD 20-JUL-2000.
 XX
 PF 11-JAN-2000; 2000MO-AU00011.
 XX
 PR 11-JAN-1999; 99AU-0008103.
 XX
 PA (UNIX) UNISEARCH LTD.
 PA (JOHN) JOHNSON & JOHNSON RES PTY LTD.
 XX
 PI Atkins DG, Baker AR, Khachigian LM;
 XX
 DR WPI; 2000-476054/41.
 XX
 PT DNazyme for treating conditions associated with proliferation or
 PT migration of cells e.g. post-angioplasty restenosis, vein graft failure
 PT and hypertension cleaves mRNA molecules encoding Egr-1 -
 XX
 PS Disclosure; Page 5; 62pp; English.
 XX
 CC Egr-1 (also known as Egr-1 and NGFI-A) is a transcription factor. Egr-1
 CC binds to the promoters of genes whose products influence cell movement
 CC and replication in the artery wall. DNA-based enzymes (DNazymes) have
 CC been developed in the present invention, which can cut Egr-1 mRNA with
 CC high efficiency and specificity, resulting in Egr-1 activity inhibition
 CC in vascular smooth muscle cells. The DNazymes can be used to inhibit
 CC EGR-1 activity in cells, inhibit proliferation or migration of cells and
 CC to treat a condition associated with cell proliferation or migration e.g.

CC post-angioplasty restenosis, vein graft failure, transplant coronary
 CC disease and complications associated with atherosclerosis e.g.
 CC cerebrovascular infarction (stroke), myocardial infarction (heart
 CC attack), hypertension or peripheral vascular disease e.g. gangrene of the
 CC extremities. The cells which are treated are vascular cells, preferably
 CC smooth muscle or endothelial cells or cells involved in neoplasia. The
 CC present sequence is rat AS2. This sequence was used to assay the activity
 CC of the DNazymes of the present invention.
 XX
 SQ Sequence 15 BP; 1 A; 6 C; 4 G; 4 T; 0 other;
 Query Match 100.0%; Score 15; DB 21; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTGGCCGCTGCCAT 15
 DB 1 CTTGGCCGCTGCCAT 15
 RESULT 3
 AAF85119
 ID AAF85119 standard; DNA; 15 BP.
 AC AAF85119;
 XX
 DT 09-JUL-2001 (first entry)
 XX
 DE Antisense oligonucleotide which targets an EGR gene.
 XX
 KM Early growth response factor; EGR; tumour cell; tumour; DNazyme;
 KM antisense oligonucleotide; prostate tumour; hepatocellular carcinoma;
 KM skin carcinoma; breast tumour; ss.
 XX
 OS Synthetic.
 XX
 PN WO200130394-A1.
 XX
 PD 03-MAY-2001.
 XX
 PF 26-OCT-2000; 2000MO-AU01315.
 XX
 PR 26-OCT-1999; 99AU-0003676.
 XX
 PA (UNIX) UNISEARCH LTD.
 PA Khachigian LM;
 XX
 PI WPI; 2001-300428/31.
 XX
 DR Treating tumors including prostate tumour, breast tumour, skin carcinoma,
 DR comprises administering agent which inhibits induction or decreases
 DR expression of early growth response factor-1 -
 XX
 PS Claim 8; Page 49; 80pp; English.
 XX
 CC The present sequence represents an antisense oligonucleotide, which
 CC targets an early growth response factor (EGR) gene. The specification
 CC describes a method for inhibiting the growth or proliferation of a tumour
 CC cell and treating tumours. The method comprises contacting a tumour cell
 CC or administering to a subject, an agent which inhibits induction,
 CC decreases expression or which decreases the nuclear accumulation or
 CC activity of EGR. The agent is a DNazyme or an antisense oligonucleotide.
 CC The method is useful for treating solid tumours, including prostate
 CC tumours, hepatocellular carcinoma, skin carcinoma or breast tumours.
 XX
 SQ Sequence 15 BP; 1 A; 6 C; 4 G; 4 T; 0 other;
 Query Match 100.0%; Score 15; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTGGCCGCTGCCAT 15

ATTORNEY/AGENT INFORMATION:
NAME: Corider, Timothy S.
REGISTRATION NUMBER: 38,414
REFERENCE/DOCKET NUMBER: UROC:007
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 474-7577
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-626-169-12

Query Match
Best Local Similarity 89.3%; Score 13.4; DB 2; Length 25;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 15 CTGGCCGCGGCCCAT 1

RESULT 9
US-09-164-907-12/c
Sequence 12, Application US/09164907A
Patent No. 6090559
GENERAL INFORMATION:
APPLICANT: RUSSELL, DAVID W.
APPLICANT: THIGPEN, ANICE E.
TITLE OF INVENTION: BIOMARKERS FOR DETECTION, DIAGNOSIS AND PROGNOSIS OF
TITLE OF INVENTION: PROSTATE CANCER
FILE REFERENCE: UROC:021
CURRENT APPLICATION NUMBER: US/09/164,907A
CURRENT FILING DATE: 1998-10-01
EARLIER APPLICATION NUMBER: 08/626,169
EARLIER FILING DATE: 1996-03-29
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 12
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-09-164-907-12

Query Match
Best Local Similarity 89.3%; Score 13.4; DB 3; Length 25;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 15 CTGGCCGCGGCCCAT 15

RESULT 10
US-08-760-075A-15/c
Sequence 15, Application US/08760075A
Patent No. 5942429
GENERAL INFORMATION:
APPLICANT: KIRSCHBAUM, Bernd
APPLICANT: MUELLNER, Stefan
APPLICANT: BARTLETT, Robert
TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,075A
FILING DATE: 04-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 19545126.0
FILING DATE: 04-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/309
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 612 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..612
FEATURE:
NAME/KEY: mat-peptide
LOCATION: 1..612
US-08-760-075A-15

Query Match
Best Local Similarity 89.3%; Score 13.4; DB 2; Length 612;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 339 CTGGCCGCGTGACAT 325

RESULT 11
US-09-338-546-15/c
Sequence 15, Application US/09338546
Patent No. 6251645
GENERAL INFORMATION:
APPLICANT: KIRSCHBAUM, Bernd
APPLICANT: MUELLNER, Stefan
APPLICANT: BARTLETT, Robert
TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/338,546
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/760,075
FILING DATE: 04-DEC-1996
APPLICATION NUMBER: DE 19545126.0
FILING DATE: 04-DEC-1995

RESULT 14
US-08-855-714-1
; Sequence 1, Application US/08855714
; Patent No. 5939075
; GENERAL INFORMATION:
; APPLICANT: Houns, Huo-Shu H.
; APPLICANT: Warren, Richard L.
; TITLE OF INVENTION: MUTANTS OF BRUCELLA MELITENSIS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran, Esq.
; STREET: HQ USAMRDC, Dept. of Army, Fort Detrick
; CITY: Frederick
; STATE: MD
; COUNTRY: US
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/855,714
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/334,129
; FILING DATE: 04-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: 08/143,692
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1920 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: BRUCELLA MELITENSIS
; US-08-855-714-1
Query Match 89.3%; Score 13.4; DB 2; Length 1920;
Best Local Similarity 93.3%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CTTGGCCGCTGCCAT 15
DB 409 CATGGCCGCTGCCAT 423
RESULT 15
US-07-872-644-5
; Sequence 5, Application US/07872644
; Patent No. 5389527
; GENERAL INFORMATION:
; APPLICANT: Beavo, Joseph A.
; APPLICANT: Bentley, Kelley
; APPLICANT: Charbonneau, Harry
; APPLICANT: Sonnenburg, William K.
; TITLE OF INVENTION: DNA Encoding Mammalian
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/872,644
; FILING DATE: 19920420
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/688,356
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5389527and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/30822
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2291 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 100..1689
; US-07-872-644-5
Query Match 89.3%; Score 13.4; DB 1; Length 2291;
Best Local Similarity 93.3%; Pred. No. 2.7e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CTTGGCCGCTGCCAT 15
DB 858 CTTGGCCGCTGCCAT 872

Search completed: December 16, 2002, 14:16:48
Job time : 69 secs

directionally ligated into the Uni-ZAP XR vector from
Stratagene and packaged using GigaPack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-ZAP phage using Ex-Assist
helper phage and propagated in XL04R cells. Note: EST may
be of fungal origin."

BASE COUNT 120 a 74 c 112 g 112 t

Query Match 100.0%; Score 15; DB 12; Length 418;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCCCGCTGCCAT 15
|||||
Db 275 CTTGCCCGCTGCCAT 261

RESULT 9
B0140289/c

LOCUS B0140289 421 bp mRNA linear EST 26-APR-2002
DEFINITION NF034A02PH1017 Phoma-infected Medicago truncatula cDNA clone
NF034A02PH 5', mRNA sequence.

ACCESSION B0140289
VERSION B0140289.1 GI:20276415
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.

1 (bases 1 to 421)
Watson,B.S., Shih,H.-S., Lopez-Meyer,M., Scott,A.D., Harris,A.R.,
Gonzales,R.A., Bell,C.J., Imman,J.T., Maugh,M.E., Sullivan,J.P.,
May,G.D. and Patra,N.L. Immun.J.T., Maugh,M.E., Sullivan,J.P.,
May,G.D. and Patra,N.L.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula Phoma-infected library
Unpublished (2002)
Contact: Patra NL
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7317
Fax: 580 221 7380
Email: nlpatra@noble.org
Insert Length: 421 Std Error: 0.00
Plate: 034 row: A column: 02
Seq primer: TCACACAGGAAACACCTATGAC.

FEATURES

Source

1..421
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone_11b="Phoma-infected"
/tissue_type="leaf"
/dev_stage="Pathogen-induced, Young trifoliolate"
/note="Vector: pBluescript SK(-); Young trifoliolate leaves
of Medicago truncatula were excised and dip-inoculated in
a spore suspension of Phoma medicaginis, and incubated in
humid dishes. Pools of leaves were harvested at 0, 15, and
30 minutes and 1, 2, 3, 6, 14, 24, 48, 72, and 96, hours,
and used to prepare total RNA. cDNA was prepared from
polyA+ enriched, pooled samples of equivalent amounts of
total RNA from each sample. The cDNA was directionally
ligated into the Uni-ZAP XR vector (Stratagene) and
packaged using the GigaPack III Gold packaging extracts.
Phagemids containing cDNA inserts were in vivo excised
from the recombinant Uni-ZAP XR vector using Ex-Assist
helper phage and the E. coli strain XL1-Blue MRF'
(Stratagene). Excised plasmids were plated using SOIR
cells."

BASE COUNT

121 a 84 c 98 g 116 t 2 others

ORIGIN

Query Match 100.0%; Score 15; DB 14; Length 421;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCCCGCTGCCAT 15
|||||
Db 360 CTTGCCCGCTGCCAT 346

RESULT 10
AW911108/c

LOCUS AW911108 426 bp mRNA linear EST 25-MAY-2000
DEFINITION ur82g09.y1 NCI-CGAP Mam6 Mus musculus cDNA clone IMAGE:3156832 5',
similar to gb:M20157 Mouse Egr-1 mRNA, complete cds (MOUSE);, mRNA
sequence.

ACCESSION AW911108
VERSION AW911108.1 GI:8076354
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 426)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/lresources.shtml

MG1:1059588
Seq primer: -40RP from Gibco
High quality sequence stop: 400.
Location/Qualifiers

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/strain="FVB/N"
/db_xref="taxon:10090"
/clone_11b="IMAGE:3156832"
/clone_11b="NCI-CGAP Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: PCMV-SpORf6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"

BASE COUNT 86 a 150 c 127 g 63 t

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Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGCCCGCTGCCAT 15
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Db 136 CTTGCCCGCTGCCAT 122

RESULT 11
LOCUS AW207985 429 bp mRNA linear EST 07-SEP-2000
DEFINITION M11006e DSIR Medicago truncatula cDNA clone IR58, mRNA sequence.

DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/BLN at:
www.bio.lnl.gov/dbp/image/image.html

MGI:1024625
 Seq primer: -40RP from 61bco
 High quality sequence stop: 413.
 Location/Qualifiers

FEATURES

source

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 /db_xref="taxon:10090"
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 /sex="female, virgin"
 /tissue_type="infiltrating ductal carcinoma"
 /dev_stage="5 months"
 /lab_host="DH10B"
 /note="Organ: mammary; Vector: PCMV-SPORT6; Site_1: SalI;
 Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
 Library constructed by Life Technologies. Investigator
 providing samples: Jeffrey Green, M.D., NIH"
 BASE COUNT 75 a 182 c 122 g 64 t
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 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGGCCGCTGCCAT 15

Db 253 CTTGGCCGCTGCCAT 239

RESULT 14

BI272170/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 451)
 Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
 Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.
 Expressed Sequence Tags from the Samuel Roberts Noble Foundation
 Medicago truncatula flower library
 Unpublished (2001)
 Contact: May GD
 Plant Biology Division
 The Samuel Roberts Noble Foundation
 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
 Tel: 580 221 7391
 Fax: 580 221 7380
 Email: gdmay@noble.org
 Insert Length: 451 Std Error: 0.00
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 Location/Qualifiers
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 /db_xref="taxon:3880"
 /clone_11b="NF021E02FL"
 /clone_11b="Developing flower"
 /tissue_type="Developing flowers"
 /dev_stage="Developmentally pooled. Contains a mixture of

BASE COUNT 133 a 83 c 112 g 122 t 1 others
 ORIGIN

Query Match 100.0%; Score 15; DB 13; Length 451;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGGCCGCTGCCAT 15

Db 335 CTTGGCCGCTGCCAT 321

RESULT 15

BB862529/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 459)
 Akimura,T., Arakawa,T., Carinici,P., Furuno,M., Hanagaki,K., Ishii
 Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii
 Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
 Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.,
 Saito,R., Sakai,C., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,
 Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suuki,H., Tagawa
 A., Takahashi,F., Takaku-Ahikita,S., Tanaka,T., Tomaru,A., Toyu,T.,
 Watabiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
 Riken Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
 2001)
 Unpublished (2001)
 Contact: Yoshinori Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center(GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suenro-cho, Tsunumi-Ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsr.riken.go.jp/
 URL: http://genome.gsc.riken.go.jp/
 Carinici,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
 M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 Wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
 Mataliki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura
 S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
 Hayashizaki,Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carinici,P., Sugahara
 Y. and Hayashizaki,Y.
 Computer-based methods for the mouse full-length cDNA

very young, developing, fully-opened flowers and flowers
 in early transition into pods."
 /note="Vector: Lambda Zap; cDNA was prepared from polyA+
 enriched, pooled samples of equivalent amounts of total
 RNA from very young, developing, fully-opened flowers and
 flowers transitioned into pods. The cDNA was
 directionally ligated into the Uni-Zap XR vector
 (Stratagene) and packaged using the GigaPack III Gold
 packaging extracts. Phagemids containing cDNA inserts were
 in vivo excised from the recombinant Uni-Zap XR vector
 using Exassist helper phage and the E. coli strain
 XL1-Blue MRF' (Stratagene). Excised plasmids were plated
 using SOLR cells."

KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
 KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
 KW hypertension; hypothyroidism; cholesterol ester storage disease;
 KW immune deficiency; immune disorder; infectious disease;
 KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
 KW myasthenia gravis; gene; ss.
 OS Homo sapiens.
 XX W0200192523-A2.
 PN 06-DEC-2001.
 PD 29-MAY-2001; 2001WO-US10836.
 XX 29-MAY-2000; 2000US-206132P.
 PR 30-MAY-2000; 2000US-206132P.
 XX 29-AUG-2000; 2000US-228716P.
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shinkets RA, Leach MD;
 XX WPI; 2002-106308/14.
 DR P-PSDB; ABP01278.
 XX
 PT Novel human polypeptides and polynucleotides useful for diagnosing,
 PT preventing and treating cardiovascular disease, neurodegenerative,
 PT hyperproliferative disorders and autoimmune disorders
 PS
 PS Disclosure; SEQ ID 2537; 1037bp; English.
 XX
 CC The present invention describes substantially purified human proteins
 CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
 CC in the specification). ABN15762 to ABN27252 encode the human ORFX
 CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
 CC treating or preventing a pathology associated with an ORFX-associated
 CC disorder in humans, and in the manufacture of a medicament for treating a
 CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
 CC sequences can be used in gene therapy. ORFX sequences can be used in the
 CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
 CC psoriasis, benign tumors, keloid, degenerative disorders, haemorrhage,
 CC osteoarthritis, neurodegenerative disorders, disorders related to organ
 CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
 CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
 CC storage disease, various immune deficiencies and disorders, infectious
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
 CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
 CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
 CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
 CC bone degenerative disorders, or periodontal disease, and for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues and conditions resulting from
 CC systemic cytokine damage.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 501 BP; 81 A; 139 C; 177 G; 104 T; 0 other;
 Query Match 93.3%; Score 14; DB 24; Length 501;
 Best Local Similarity 100.0%; Pred. No. 7.5e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CTTGGCCGCTGCCA 14
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 Db 310 CTTGGCCGCTGCCA 297

Search completed: December 16, 2002, 12:41:33
 Job time : 304 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 16, 2002, 12:41:44 ; Search time 89 Seconds

(without alignments)
66,651 Million cell updates/sec

Title: US-09-648-389A-1

Sequence: 1 cttggccgcgtccat 15

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Gapop 10.0 , Gapext 1.0

Searched: 355320 seqs, 197730502 residues

Total number of hits satisfying chosen parameters: 710640

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	15	100.0	433	US-09-960-352-1555	Sequence 1555, Ap
2	15	100.0	3112	US-09-917-800A-1543	Sequence 1543, Ap
3	13.4	89.3	152	US-09-974-300-5464	Sequence 5464, Ap
4	13.4	89.3	157	US-09-864-761-27552	Sequence 27552, A
5	13.4	89.3	255	US-09-864-761-20348	Sequence 20348, A
6	13.4	89.3	255	US-09-864-761-11839	Sequence 31839, A
7	13.4	89.3	265	US-09-923-876-2313	Sequence 2313, Ap
8	13.4	89.3	273	US-09-923-876-4805	Sequence 4805, Ap
9	13.4	89.3	349	US-09-960-352-1856	Sequence 1856, A
10	13.4	89.3	414	US-09-960-352-11961	Sequence 11961, A
11	13.4	89.3	425	US-09-960-352-10722	Sequence 10722, A
12	13.4	89.3	454	US-09-864-761-3580	Sequence 3580, Ap
13	13.4	89.3	454	US-09-864-761-16568	Sequence 16568, A
14	13.4	89.3	480	US-09-864-761-10916	Sequence 10916, A
15	13.4	89.3	480	US-09-974-300-5449	Sequence 5449, Ap
16	13.4	89.3	579	US-09-864-761-15317	Sequence 15317, A
17	13.4	89.3	681	US-09-815-242-6787	Sequence 6787, Ap
18	13.4	89.3	775	US-09-910-943-62	Sequence 62, Appl
19	13.4	89.3	1026	US-09-974-300-6635	Sequence 6635, Ap

20	13.4	89.3	1593	US-09-814-777A-31	Sequence 31, Appl
21	13.4	89.3	1926	US-10-024-632-5	Sequence 5, Appl1
22	13.4	89.3	2291	US-09-883-825-5	Sequence 5, Appl1
23	13.4	89.3	2656	US-09-883-825-16	Sequence 16, Appl
24	13.4	89.3	3132	US-09-736-457-320	Sequence 320, Appl
25	13.4	89.3	3132	US-09-902-941-320	Sequence 320, Appl
26	13.4	89.3	3132	US-09-880-107-3721	Sequence 3721, Ap
27	13.4	89.3	3984	US-09-954-531-151	Sequence 151, Appl
28	13.4	89.3	4021	US-10-002-600-40	Sequence 40, Appl
29	13.4	89.3	4559	US-09-919-172-61	Sequence 61, Appl
30	13.4	89.3	4559	US-10-044-090-555	Sequence 555, Appl
31	13.4	89.3	12421	US-09-989-920-128	Sequence 128, Appl
32	13.4	89.3	15747	US-09-070-927A-81	Sequence 81, Appl
33	13.4	89.3	17082	US-09-070-927A-229	Sequence 229, Appl
34	13.4	89.3	25	US-09-840-479-30	Sequence 30, Appl
35	13.4	89.3	31	US-09-801-274-580	Sequence 580, Appl
36	13.4	89.3	271	US-09-878-574-11159	Sequence 11159, A
37	13.4	89.3	272	US-09-923-876-1383	Sequence 1383, Ap
38	13.4	89.3	324	US-09-920-300A-632	Sequence 632, Appl
39	13.4	89.3	324	US-10-033-528-632	Sequence 632, Appl
40	13.4	89.3	324	US-10-033-528-961	Sequence 961, Appl
41	13.4	89.3	324	US-10-033-528-961	Sequence 961, Appl
42	13.4	89.3	393	US-09-960-352-10566	Sequence 10566, A
43	13.4	89.3	408	US-09-960-352-8849	Sequence 8849, Ap
44	13.4	89.3	445	US-09-764-864-598	Sequence 598, Appl
45	13.4	89.3	468	US-10-046-935-606	Sequence 606, Appl

ALIGNMENTS

RESULT 1
US-09-960-352-1555/c
Sequence 1555 Application US/09960352
Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathaiagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION A
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 1555
LENGTH: 433
TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 07-LIB34-039-Q1-EL-B3
US-09-960-352-1555

Query Match 100.0%; Score 15; DB 10; Length 433;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTGGCCGCGTCCAT 15
DB 24 CTTGGCCGCGTCCAT 10

RESULT 2
US-09-917-800A-1543/c
Sequence 1543 Application US/09917800A
Patent No. US20020119462A1
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Castelle, Arthur
APPLICANT: Elashoff, Michael
APPLICANT: Gene Logic, Inc.

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/040,548
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Coughlin, Daniel F.
REGISTRATION NUMBER: 36,111
REFERENCE/DOCKET NUMBER: arc0067
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 744-0090
TELEFAX: (312) 245-4961
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 843 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-040-548-9

Query Match 100.0%; Score 15; DB 1; Length 843;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGGCCGCTGCCAT 15
DB 15 CTGGCCGCTGCCAT 1

RESULT 3
US-08-466-344-9/c
Sequence 9, Application US/08466344
Patent No. 5773583
GENERAL INFORMATION:
APPLICANT: Sukhatme, Vikas P.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE
NUMBER OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: 321 No. 5773583th Clark Street, Suite 800
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60610
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,344
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/040,548
FILING DATE: 31-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Coughlin, Daniel F.
REGISTRATION NUMBER: 36,111
REFERENCE/DOCKET NUMBER: arc0067
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 744-0090
TELEFAX: (312) 245-4961
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 843 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-08-466-344-9

Query Match 100.0%; Score 15; DB 1; Length 843;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGGCCGCTGCCAT 15
DB 15 CTGGCCGCTGCCAT 1

RESULT 4
US-08-224-482-1/c
Sequence 1, Application US/08224482
Patent No. 5837692
GENERAL INFORMATION:
APPLICANT: Mercola, Dan
ATTORNEY/AGENT INFORMATION:
NAME: Adamson, Eileen D.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: PDGF by Mammalian EGR
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/224,482
FILING DATE: 07-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-ME 9913
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3068 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 370..1858
US-08-224-482-1

Query Match 100.0%; Score 15; DB 2; Length 3068;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CTGGCCGCTGCCAT 15
DB 273 CTGGCCGCTGCCAT 259

RESULT 5
US-08-040-548-15/c
Sequence 15, Application US/08040548
Patent No. 5763209
GENERAL INFORMATION:
APPLICANT: Sukhatme, Vikas P.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO THE
NUMBER OF INVENTION: FUNCTIONAL DOMAINS OF DNA BINDING PROTEINS
NUMBER OF SEQUENCES: 67

OY 1 CTGGCGCGTGCAT 15
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DB 142 CTGGCGCGTGCAT 156

RESULT 5
US-09-864-761-20348/c
Sequence 20348, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aecomica-X-1
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US/09/864,761
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 20348
LENGTH: 255
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC007263.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.79
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.6
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.76
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.77
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.88
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.92

OTHER INFORMATION: NT HIT: X74507.1, EVALU 6.10e-01
OTHER INFORMATION: SWISSPROT HIT: P56558, EVALU 8.70e+00
US-09-864-761-20348

Query Match 89.3%; Score 13.4; DB 10; Length 255;
Best Local Similarity 93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CTGGCGCGTGCAT 15
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DB 104 CTGGCGCGTGCAT 90

RESULT 6
US-09-864-761-31839/c
Sequence 31839, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
FILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aecomica-X-1
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US/09/864,761
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 31839
LENGTH: 255
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC007263.4
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 8.5

Best Local Similarity 93.3%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CTTGGCGCTGCCAT 15
|||||||
Db 49 CTTGGCGATGCCAT 35

Search completed: December 16, 2002, 14:18:28
Job time : 89 secs



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Indexing Officer: MTSEGABRHAM - MEAREG TSEGABRHAM
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Dossier: 09648389

Legal Date: 03-12-2003

No.	Doccode	Number of pages
1	LET.	3

Total number of pages: 3

Remarks:

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